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(54) Title: COLLECTION OF PROKARYOTIC DNA FOR TWO HYBRID SYSTEMS *HELICOBACTER PYLORI* PROTEIN-
PROTEIN INTERACTIONS AND APPLICATION THEREOF

(57) Abstract: The present invention concerns collections of recombinant cell clones derived from a prokaryotic genome, more particularly from *Helicobacter pylori* genome, usable for two-hybrid systems and methods to produce such collections. The invention further relates to the identification of *H. pylori* protein-protein interactions and to the application of said collections of recombinant cell clones and said identified proteins interactions to the pharmaceutical and diagnostic field.

AMENDED CLAIMS

[received by the International Bureau on 28 November 2000 (28.11.00);
original claim 60 amended; remaining claims unchanged (2 pages)]

- b) a polynucleotide having the sequence identified by the reference indicated in the right column "SID®" in table III ;
- c) fragment having at least 12 consecutive nucleotides of polynucleotide of a) or b), complement thereof, and RNA corresponding to said polynucleotide ; and
- 5 d) a polynucleotide having at least 80 % identity degree after alignment to a nucleic acid sequence of a polynucleotide of a) or b) ;
- with the exception of the polynucleotides encoding the polypeptide having the sequence disclosed in the EMBL Data base document Accession number 025045.

61. Purified or isolated polypeptide selected from the group consisting of :

- 10 a) a polypeptide having an amino acids sequence identified by the reference indicated in the right column "SID®" in table II, and fragment thereof having at least 5 consecutive amino acids ; and
- b) a polypeptide encoded by a polynucleotide according to claim 59 or 60.

62. Use of a polynucleotide according to claim 60 as a primer for
15 amplification.

63. Use of a polynucleotide according to claim 60 as a specific probe for detection.

64. Cloning or expression vector containing a polynucleotide according to anyone of claims 59 and 60.

20 65. Vector according to claim 64, wherein the vector is the plasmid pACT11st, pAS2ΔΔ or pP6.

66. Vector according to claim 64, wherein the vector is the plasmid selected from the group consisting of pT25, pKT25, pUT18 and pUT18C.

67. Vector according to claim 64, wherein the vector is self replicated.

25 68. Vector according to claim 64 or 67, wherein the vector is a viral vector.

69. Vector according to claim 68, wherein the vector is chosen between an adenovirus, AAV, a retrovirus, a proxivirus or an herpes virus.

70. Vector according to anyone of claims 64 to 69 including elements allowing expression and/or secretion of said polynucleotide in a host cell.

30 71. Host cell transformed with a vector according to anyone of claims 64 to 70.

72. Host cell according to claim 71, wherein the host cell is a prokaryotic cell.

73. Host cell according to claim 71, wherein the host cell is an eukaryotic cell.

5 74. Method for producing a polypeptide according to anyone of claims 45 and 61, comprising the steps of :

- a) cultivating a host cell according to anyone of claims 71 to 73 under conditions and in culture medium allowing the growth of said host cell and the expression of said polypeptide; and
- 10 b) recovering said polypeptide directly from the culture medium or from said cultivated cell obtained in step a).

75. Purified or isolated polypeptide obtained by the method according to claim 74.

15 76. A method for selecting an agent capable of modulating the protein-protein interaction of a step of two polypeptides according to claim 45 comprising the steps of :

- a) cultivating a recombinant cell clone containing a reporter gene expression of which is toxic for said recombinant cell clone and transformed with two plasmids wherein :
 - 20 i) the first plasmid contains a nucleic construct comprising a nucleic sequence encoding a first hybrid polypeptide containing one of said two polypeptides and a DNA binding domain ;
 - ii) the second plasmid contains a nucleic construct comprising a nucleic sequence encoding a second hybrid polypeptide containing the second of said two polypeptides and an activating domain capable of activating said toxic reporter gene when the first
 - 25 and the second hybrid polypeptides are interacting ;
- on a selective medium containing the agent to be tested and allowing the growth of said recombinant cell clone when the toxic reporter gene is not activated ; and
- b) selecting agent which is capable of inhibiting the growth of the recombinant cell clone cultivated in step a).

30 77. A method for selecting an agent capable of modulating the protein-protein interaction of a set of two polypeptides according to claim 45 comprising the steps of :

specific site on the DNA and a domain that is necessary for activation (Keegan et al., 1986, Science, 231(4739): 699-704 Separation of DNA binding from the transcription activating function of eukaryotic regulatory protein).

To date however, the two-hybrid assay system has not been specifically applied to
5 the systematic study of prokaryotic protein-protein interactions although number of diseases are due to prokaryotic microorganisms.

One of the prokaryotic microorganisms presenting a great interest is *Helicobacter pylori*. *Helicobacter pylori* (*H. pylori*) is a microaerophilic, Gram negative, slow growing, spiral shaped and flagellated organism. *H. pylori* has been first isolated in
10 1983 from gastric biopsy specimen of patient with chronic gastritis (Marshall et al., 1984, Lancet, i:1311-1314, Unidentified curved bacilli in the stomach of patients with gastritis and peptic ulceration).

Helicobacter pylori has become identified as a primary cause of chronic gastroduodenal disorders, such as gastritis, dyspepsia, and peptic ulcers, in humans.
15 Studies have shown (Labigne et al.) that *H. pylori* can be successfully eradicated by a treatment combining two antibiotics with a proton pump inhibitor. However, few antibiotics are active against *H. pylori*, and antibiotic-resistant strains have begun to appear.

H. pylori strain n° 26695 genome has been studied by Tomb et al. (Tomb et al.,
20 1997, Nature, vol. 388, 539-547, The complete genome sequence of the gastric pathogen *Helicobacter pylori*). This strain's genome consists of a circular chromosome with a size of 1,667,867 bp, average G + C content of 39 %, and 1590 predicted coding sequences (open reading frames or "ORF").

The bacterial factors necessary for colonization of the gastric environment, and
25 for virulence of this pathogen, are poorly understood. Examples of known virulence factors are :

- Enzymes involved in neutralizing the acid gastric pH : the multisubunit urease is a characteristic enzyme that is crucial for survival in acidic pH and for successful colonization of the gastric environment, a site that few other microbes can colonize
30 (Labigne et al., WO 93/07273, *Helicobacter pylori* genes necessary for the regulation and maturation of urease, and use thereof). Genes encoding ureases have been located

on a 34 kb chromosome fragment and comprise ureA, ureB, ureC, ureD, ureE, ureF, ureG, ureH and ureI.

- Bacterial flagellar proteins responsible for motility across the mucous layer (Hazell et al., 1986, J. Inf. Dis., 153, 658-663 *Campylobacter pyloridis and gastritis* : association with intracellular spaces and adaptation to an environment of mucus as important factors in colonization of the gastric epithelium; Leying et al., 1992, Mol. Microbiol., 6, 2863-2874 Cloning and genetic characterization of *Helicobacter pylori* flagellin gene) : flagellar filaments biosynthesis comprises A and B flagellins and the filament cap. These two biosyntheses are regulated by flbA gene (Suerbaum et al., French patent application, 1995, N 2 736 360, Cloning and characterization of flbA gene of *Helicobacter pylori*, aflagellated strains production).

- Two other essential toxins for virulence are VacA and CagA :

- VacA is a *H. pylori* toxin that induces the formation of large acidic vacuoles in host epithelial cells. These large vacuoles originate from massive swelling of membranous compartments of late stages of the endocytic pathway (de Bernard et al., 1997, Microbiology, 26(4), 665-674, *Helicobacter pylori* toxin VacA induces vacuole formation by acting in the cell cytosol). Proof for receptor-mediated interaction with VacA has been made by Pagliaccia et al.; m2 allele of vacA gene has always been described as inactive in the in vitro HeLa cell assay, however, the m2 allele is associated with peptic ulcer and is prevalent in populations in which peptic ulcer and gastric cancer have high incidence (Pagliaccia et al., Proc. Natl. Acad. Sci. U.S.A., 1998, 95(17), 10212-10217, The m2 form of the *Helicobacter pylori* cytotoxin has cell type-specific vacuolating activity).

- CagA is one of the proteins encoded by the "cag pathogenicity island" (Spohn et al. 1997, Molecular Microbiology, 26(2), 361-372, Transcriptional analysis of the divergent cagAB genes encoded by the pathogenicity island of *Helicobacter pylori*) found in *H. pylori* strains isolated from most patients with peptic ulcer disease and adenocarcinoma. CagA is produced by 50-60 % of *H. pylori* strains; it is a high molecular weight (120-140 kDa) superficial protein and an immunodominant antigen with unknown function. *H. pylori* strains that produce CagA protein have two genes cagB and cagC (36 and 101 kDa proteins, respectively). These genes are highly

associated with duodenal ulcers (Blaser et al. 1996, WO 96/12825, *cagB* and *cagC* genes of *Helicobacter pylori* and related methods and compositions).

- Other virulence factors are : several gastric tissue-specific adhesins (Boren et al., 1993, Science, 262, 1892-1895).

5 Therapeutic agents are currently available that eradicate *H. pylori* infections *in vitro*. However, methods employing antibiotic agents result in the emergence of bacterial strains which are resistant to these agents.

As number of diseases are due to prokaryotic microorganisms, there is a great need for new tools directed to the functional and global study of these newly
10 characterized complete or partial genome, particularly *Escherichia coli* genome, but also of pathogenic microorganisms such as *H. pylori*, *Staphylococcus aureus* and *Streptococcus pneumoniae* genomes.

In addition to the need for these new tools, there is also and especially a need to find new *E. coli*, *H. pylori*, *S. aureus* and *S. pneumoniae* protein-protein interactions for
15 the development of more effective and better targeted therapeutic.

Summary of the invention

The present invention relates to a method for producing a collection of recombinant cell clones usable for two-hybrid systems containing genomic DNA
20 fragments of prokaryotic micro-organism, particularly of *E. coli*, *H. pylori*, *S. aureus* and *S. pneumoniae*, to collection of recombinant cell clones obtainable by this method and kit for screening comprising said collection.

The invention is also directed to a yeast or bacterial two-hybrid system method for identifying a recombinant cell clone expressing a prey polypeptide of a prokaryotic
25 microorganism capable of interacting with a bait polypeptide and a method for identifying said prey polypeptide.

The present invention further comprises polynucleotides or polypeptides corresponding to the prey polypeptides capable of interacting with a bait polypeptide and the protein-protein interactions identified by the yeast or bacterial two-hybrid
30 system method according to the invention, vectors and host cells containing said polynucleotides, and pharmaceutical composition including them.

The present invention also concerns a method for identifying a polynucleotide encoding a selected interacting domain (SID®) of a prey polypeptide of interest from a prokaryotic microorganism capable of interacting with a bait polypeptide.

Another aspect of the present invention relates to a method for selecting an agent
5 capable of modulating the protein-protein interaction identified by the yeast or bacterial two-hybrid system method according to the invention.

Brief description of the drawings

Figure 1 is a restriction map of the plasmid pAS2ΔΔ which may be used for the
10 yeast two-hybrid system.

Figure 2 is a restriction map of the plasmid pACT11st which may be used for the yeast two-hybrid system.

Figure 3 is a restriction map of the plasmid pUT18 which may be used for the bacterial two-hybrid system. In this figure, each multicloning site (MCS) is detailed.

Figure 4 is a restriction map of the plasmid pUT18C which may be used for the
15 bacterial two-hybrid system. In this figure, each multicloning site (MCS) is detailed.

Figure 5 is a restriction map of the plasmid pT25 which may be used for the bacterial two-hybrid system. In this figure, each multicloning site (MCS) is detailed.

Figure 6 is a restriction map of the plasmid pKT25 which may be used for the
20 bacterial two-hybrid system. In this figure, each multicloning site (MCS) is detailed.

Figure 7 is a schematic representation of the SID® identification method. In this figure, the « Full-length prey protein » is the Open Reading Frame where the identified prey polypeptides are included, the Selected Interaction Domain SID® is determined by comparison of every prey polypeptide fragment.

Figure 8 is a restriction map of the plasmid pP6 which may be used for the yeast
25 two-hybrid system.

Detailed description of the invention

The present invention is directed to a method for producing a collection of
30 recombinant cell clones usable for two-hybrid systems comprising the steps of :

a) fragmenting DNA ;

b) inserting polynucleotidic fragments obtained in step a) in plasmids in such a way that the expression of said plasmids in host cell leads to an hybrid polypeptide containing a specific domain capable of activating a reporter gene when associated with a complementary domain ;

5 c) transforming cell clones with plasmids obtained in step b); and

d) optionally, selecting the transformed recombinant cell clones obtained in step c) ;

wherein DNA of step a) is genomic DNA obtained from a prokaryotic micro-organism.

The step a) of fragmenting DNA according to the method of the invention may be obtained by enzyme digestion, sonication or nebulization of the source of genomic
10 DNA, sonication and nebulization ensuring a random cleavage of the starting DNA material and thus an excellent representation of all the possible inserts.

In a preferred embodiment, the step a) of fragmenting DNA of the method according to the invention is carried out by a nebulization process, for example, with a commercial nebulizer (GATC).

15 In a preferred embodiment, the plasmid used in the method for producing a collection of recombinant cell clones usable for two-hybrid systems according to the present invention may comprise in addition a nucleic sequence encoding a promoter, a multicloning site, a terminator site and a selection marker, operably linked.

A "promoter" refers to a DNA sequence recognized by the transcriptional
20 machinery of the cell required to initiate the specific transcription of a gene.

A sequence which is "operably linked" to a regulatory sequence such as a promoter means that said regulatory element is in the correct location and orientation in relation to the nucleic acid to control RNA polymerase initiation and expression of the nucleic acid of interest. As used herein, the term "operably linked" refers to a linkage of
25 polynucleotide elements in a functional relationship. For instance, a promoter or enhancer is operably linked to a coding sequence if it affects the transcription of the coding sequence. More precisely, two DNA molecules (such as a polynucleotide containing a promoter region and a polynucleotide encoding a desired polypeptide or polynucleotide) are said to be "operably linked" if the nature of the linkage between the
30 two polynucleotides does not (1) result in the introduction of a frame-shift mutation or (2) interfere with the ability of the polynucleotide containing the promoter to direct the transcription of the coding polynucleotide.

As a promoter, one could use full or truncated ADH promoter.

By specific domain, it is intended a domain whose association with a complementary domain leads to the activation of a reporter gene.

In one particular embodiment of this invention, the specific domain may be a transcriptional activating domain or a DNA-binding domain and the complementary domain may, respectively, be a DNA binding domain or a transcriptional activation domain.

Transcriptional activating domain and DNA-binding domain may be derived from Gal4 and LexA respectively.

In another particular embodiment of the invention, the activation domain is a part of an enzyme and the complementary domain is the other part of the same enzyme. Proximity of the two parts of the enzyme may restore the enzyme activity and activate a reporter gene.

For example, specific and complementary domain may be T25 and T18 polypeptides that constitute the catalytic domain of *Bordetella pertussis* adenylate cyclase.

The reporter gene may be contained either in a plasmid of recombinant cell clone or in its genome.

As an illustrative embodiment of the invention, the reporter gene is chosen among the group consisting in a nutritional gene or also a gene the expression of which is visualized by colorimetry such as His3, LacZ or both LacZ and His3.

As a selective marker, gene encoding for a toxin, color marker of the type of the Green Fluorescent Protein (GFP), gene encoding for phage receptor proteins or fragment thereof such as phage λ receptor lam B and any other gene giving selectable phenotype, resistance gene, such as ampicilline, kanamycin, tetracyclin or lactose or maltose nutritional gene, may be used.

In a particularly preferred embodiment, the invention relates to a method according to the invention wherein DNA of step a) is genomic DNA obtained from *Helicobacter pylori* (see example 1.A.), *Escherichia coli*, *Staphylococcus aureus* and *Streptococcus pneumoniae*.

The invention also concerns a collection of recombinant cell clones usable for two-hybrid systems obtainable by a method according to the invention.

The invention further concerns a collection of recombinant cell clones usable for two-hybrid systems, each recombinant cell clone containing a polynucleotide inserted in a plasmid whose expression leads to hybrid polypeptide containing a specific domain, wherein the said polynucleotide is a genomic DNA fragment obtained from a prokaryotic micro-organism.

In a preferred embodiment, said genomic DNA fragment is obtained by a fragmentation process by nebulization.

In a particularly preferred embodiment, the invention relates to collection of recombinant cell clones of the invention wherein the prokaryotic micro-organism is *Helicobacter pylori*, *Escherichia coli*, *Staphylococcus aureus* and *Streptococcus pneumoniae*.

The present invention also comprises a collection of recombinant cell clones according to the invention, wherein the recombinant cell clones are selected from the group consisting of Gram+ or Gram- bacteria, yeasts, fungi and mammalian cells, particularly from the group consisting of *Escherichia coli* bacteria and *Saccharomyces cerevisiae* yeast.

The present invention further concerns a collection of recombinant cell clones according to the invention, wherein the plasmids comprise at least a nucleic sequence coding a promoter, a specific domain, a multicloning site where the said polypeptide is cloned, and a selection marker.

In a preferred embodiment, the present invention further concerns a collection of recombinant cell clones according to the invention, wherein the polynucleotide is inserted in the plasmid pACT11st or in the plasmid pP6.

In a more preferred embodiment, the present invention further concerns a collection of recombinant cell clones according to the invention, wherein the collection contains 10^6 to 10^7 or to 10^8 recombinant *Escherichia coli* clones and wherein the proportion of independent cell clones with insert is at least 60 %, 70 %, 80 %, 90 %, 95 % or 97 %.

The present invention particularly comprises the collection of recombinant cell clones according to the invention which has been deposited in the Collection National de Cultures de Microorganismes (CNCM) (France, Paris) on April 13, 1999 under the

accession number I-2181, and on March 23, 2000 under the accession numbers I-2416, I-2414, I-2415 and I-2417.

The collection of recombinant cell clones which has been deposited under the accession number I-2181 (identification reference : HGXBHP1) concerns a genomic
5 library of *Helicobacter pylori* 26695 strain, cloned in the stop bis pACTII vector, transformed in *Escherichia coli* DH10B. The collection contains about 10^7 independent clones with an insert pourcentage of about 97 % and an insert average size of 1000 pb.

The collection of recombinant cell clones which has been deposited under the accession number I-2416 (identification reference : HGXBSA1) concerns a genomic
10 library of *Staphylococcus aureus* col strain, cloned in the pP6 vector, transformed in *Escherichia coli* DH10B. The collection contains about 6.8×10^7 independent clones with an insert pourcentage superior to 95 % and an insert average size of 1100 pb.

The collection of recombinant cell clones which has been deposited under the accession number I-2415 (identification reference : HGXBEC1) concerns a genomic
15 library of *Escherichia coli* MG1655 strain, cloned in the pP6 vector, transformed in *Escherichia coli* DH10B. The collection contains about 3×10^7 independent clones with an insert pourcentage superior to 98 % and an insert average size of 853 pb.

The collection of recombinant cell clones which has been deposited under the accession number I-2417 (identification reference : HGXBHP4) concerns a genomic
20 library of *Helicobacter pylori* 26695 strain, cloned in the pP6 vector, transformed in *Escherichia coli* DH10B. The collection contains about 1.9×10^7 independent clones with an insert pourcentage superior to 98 % and an insert average size of 1009 pb.

In another aspect, the present invention relates to a collection of recombinant
25 cell clones according to the invention, wherein the collection contains 10^5 to 1.5×10^7 haploid recombinant *Saccharomyces cerevisiae* clones and wherein the proportion of independant cell clones with insert is at least 60 %, 70 %, 80 %, 90 %, 95 % or 97 %.

The present invention particularly comprises the collection of recombinant cell clones according to the invention which has been deposited in the Collection National
30 de Cultures de Microorganismes (CNCM) on April 13, 1999 under the accession

number I-2182, and on March 23, 2000 under the accession numbers I-2420, I-2419 and I-2418.

The collection of recombinant cell clones which has been deposited under the accession number I-2182 (identification reference : HGXYHP1) concerns a genomic
5 library of *Helicobacter pylori*, 26195 strain, which has been amplified in *E. coli* (HGXBHP1 library), cloned in the stop bis pACTII vector, transformed in *Saccharomyces cerevisiae*, Y187 strain, and containing about $2 \cdot 10^6$ independent clones.

The collection of recombinant cell clones which has been deposited under the accession number I-2420 (identification reference : Lib Sa2) concerns a genomic
10 library of *Staphylococcus aureus*, col strain, which has been amplified in *E. coli* (HGXB SA1 library), cloned in the pP6 vector, transformed in *Saccharomyces cerevisiae*, Y187 strain, containing about $2.2 \cdot 10^6$ independent clones, and a cell concentration about $5 \cdot 10^8$ cells/ml.

The collection of recombinant cell clones which has been deposited under the
15 accession number I-2419 (identification reference : Sp in Y187 pP6) concerns a genomic library of *Streptococcus pneumoniae*, type 4 strain, which has been amplified in *E. coli* (HGXBSP1 library), cloned in the pP6 vector, transformed in *Saccharomyces cerevisiae*, Y187 strain, containing about $2.8 \cdot 10^6$ independent clones, and a cell concentration about $5 \cdot 10^8$ cells/ml.

20 The collection of recombinant cell clones which has been deposited under the accession number I-2418 (identification reference : E.coli in Y187 lib1) concerns a genomic library of *Escherichia coli*, MG1655 strain, which has been amplified in *E. coli* (HGXBEC1 library), cloned in the pP6 vector, transformed in *Saccharomyces cerevisiae*, Y187 strain, containing about $4 \cdot 10^6$ independent clones, and a cell
25 concentration about $5 \cdot 10^8$ cells/ml.

In another aspect, the present invention relates to a collection of recombinant cell clones according to the invention, wherein the polynucleotide is inserted in the plasmid pAS2ΔΔ.

Still another aspect, the present invention relates to a collection of recombinant cell clones according to the invention, wherein the polynucleotide is inserted in a plasmid selected from the group consisting of pT25, pKT25, pUT18 and pUT18C.

The present invention also relates to a kit for screening protein-protein interaction comprising a collection of recombinant cell clones usable for two-hybrid systems according to the invention.

In a particular embodiment of the collection according to the invention, the DNA library is presented as a ready to use kit for screening protein-protein interaction consisting in a collection of recombinant haploid yeast cells containing the whole genome as inserts generated during the construction of the DNA library under the form of prey polynucleotides, said collection of yeast cells being frozen in multiple vial containing an identical biological material.

The present invention also provides a generally method for selecting a polynucleotide of the collection according to the present invention, encoding a prey polypeptide, that is capable of interacting with bait polypeptide of interest.

As used interchangeably herein, the terms "polynucleotides", "nucleic acid" "oligonucleotides", include RNA, DNA, or RNA/DNA hybrid sequences of more than one nucleotide in either single chain or duplex form. The polynucleotide sequences of the invention may be prepared by any known method, including synthetic, recombinant, ex vivo generation, or a combination thereof, as well as utilizing any purification methods known in the art.

The term "purified" is used herein to describe a polynucleotide of the invention which has been separated from other compounds including, but not limited to other nucleic acids, carbohydrates, lipids and proteins. A polynucleotide is substantially pure when at least about 50 %, preferably 60 to 90 % weight/weight of a sample exhibits a single polynucleotide sequence, more usually about 95 %, and preferably is over about 99 %.

As used herein, the term "isolated" requires that the material be removed from its original environment (e.g., the natural environment if it is naturally occurring). For example, a naturally-occurring polynucleotide or polypeptide present in a living animal is not isolated, but the same polynucleotide or DNA or polypeptide, separated from some or all of the coexisting materials in the natural system, is isolated. Such

polynucleotide could be part of a vector and/or such polynucleotide or polypeptide could be part of a composition, and still be isolated in that the vector or composition is not part of its natural environment.

The term "polypeptide" refers to a polymer of amino acids without regard to the length of the polymer ; thus, peptides, oligopeptides, and proteins are included within the definition of polypeptide, these terms as used herein are interchangeable. The term "polypeptide" also does not specify or exclude post-expression modifications of polypeptides, for example, polypeptides which include the covalent attachment of glycosyl groups, acetyl groups, phosphate groups, lipid groups and the like are expressly encompassed by the term polypeptide. Also included within the definition are polypeptides which contain one or more analogs of an amino acid (including, for example, non-naturally occurring amino acids, amino acids which only occur naturally in an unrelated biological system, modified amino acids from mammalian).

The term "purified" is used herein to describe a polypeptide of the invention which has been separated from other compounds including, but not limited to nucleic acids, carbohydrates, lipids and other proteins. A purified polypeptide typically comprises about 50 %, preferably 60 to 90 % weight/weight of a protein sample, more usually about 95 %, and preferably is over about 99 % pure.

Bait polypeptide of interest is either a prokaryotic polypeptide encoded by a polynucleotide of the collection according to the present invention, or any other polypeptides of interest. Other polypeptides of interest can be polypeptides of an organism that may be infected by the prokaryotic micro-organism, for example, mammalian organism, in particular human organism.

The following described method is the mating yeast two-hybrid system and the bacterial two-hybrid system but variants of two-hybrid systems could also be used.

For example, the three hybrid system (Tirode et al., 1997, Journal of Biological Chemistry, 272, 22995-22999, A conditionally expressed third partner stabilises or prevents the formation of a transcriptional activator in a three-hybrid system) involves three polypeptides that allow or prevent the formation of the transcriptional activator. Beside the two-hybrid fusion proteins, the third partner is under the control of the Met25 promoter, which is positively regulated in medium lacking methionine. Another variant is the reverse two-hybrid system (Vidal et al., 1996, Proc. Natl. Sci., 93, 10315-

10320, Reverse two-hybrid and one-hybrid system to detect dissociation of protein-protein and DNA-protein interaction) where a collection of molecules can be screened that may inhibit a specific protein-protein interaction.

Yet another aspect, the present invention relates to yeast two-hybrid system
5 method for identifying a recombinant cell clone containing a prey polynucleotide encoding a prey polypeptide capable of interacting with a bait polypeptide comprising the steps of:

- a) mating at least one first haploid recombinant cell clone of a collection of recombinant cell clones according to the invention transformed with a plasmid
10 containing the prey polynucleotide to be assayed with a second haploid recombinant *S. cerevisiae* cell clone transformed with a plasmid containing a bait polynucleotide encoding said bait polypeptide ;
- b) cultivating diploid cell obtained in step a) on selective medium; and
- c) selecting recombinant cell clones capable of growing on selective medium.

15 In a particular embodiment, the invention is directed to a yeast two-hybrid system method for identifying a prey polynucleotide encoding a prey polypeptide capable of interacting with a bait polypeptide comprising the steps of:

- a) identifying a recombinant cell clone containing a prey polynucleotide encoding a prey polypeptide capable of interacting with a bait polypeptide according to the
20 invention ; and
- b) characterizing the prey polynucleotide contained in each recombinant cell clone selected in step a).

By yeast two-hybrid system is intended a method that usually makes use of at least one reporter gene, the transcription of which is activated when a prey polypeptide
25 and a bait polypeptide produced by recombinant cell, due to the triggering of the transcription of said at least one reporter gene when both the specific domain contained in one prey polypeptide and the complementary domain contained in the bait polypeptide are in proximity one to the other. In an advantageous variant of yeast two hybrid system, prey polynucleotides encoding for prey polypeptides and bait
30 polynucleotides encoding for bait polypeptides or proteins are inserted in recombinant haploid yeast cells, then a mating step leads to diploid yeast cells that produce the prey polypeptide and the bait polypeptide.

By at least one reporter gene according to the invention, it is intended from one to five, and preferably two or three reporter genes, the transcription of which is activated within the recombinant diploid yeast cell when the encoded bait and prey polypeptide are capable of interacting.

5 Preferably, the at least one reporter gene is contained in the first recombinant haploid yeast cell containing the bait polynucleotide.

The at least one reporter gene may be contained either in a plasmid of the recombinant diploid yeast cell or in its genome.

10 As an illustrative embodiment, the at least one reporter gene is located in the chromosome of one recombinant haploid yeast cell used according to the previously described two-hybrid system and preferably the yeast cell containing the bait polynucleotide. The at least one reporter gene can be chosen among the group consisting in a nutritional gene or also a gene the expression of which is visualized by colorimetry, such as His3, LacZ or both LacZ and His3.

15 By "prey polynucleotide", it is intended a chimeric polynucleotide encoding a chimeric polypeptide comprising i) a specific domain and ii) a polypeptide that is to be tested for interaction with a bait polypeptide. The specific domain is preferably a transcriptional activating domain.

20 The prey polynucleotide may be obtained from a genomic library of a prokaryotic micro-organism, preferably from genomic DNA of *Helicobacter pylori*.

By a "bait polynucleotide", it is intended a chimeric polynucleotide encoding a chimeric polypeptide comprising i) a complementary domain and ii) a polypeptide that is to be tested for interaction with at least one prey polypeptide. The complementary domain is preferably a DNA-binding domain that recognizes a binding site on a detectable gene that is contained in a host organism.

25 Using as the bait polynucleotide, a complete open reading frame (ORF) that may be obtained either by digestion with a restriction endonuclease (Sambrook et al., 1973, Biochemistry 12(16): 3055-63 *Detection of two restriction endonuclease activities in Haemophilus parainfluenzae using analytical agarose-ethidium bromide electrophoresis*) or by digestion with an exonuclease such as Ball, or also by DNA synthesis. The complete ORF can also correspond to a given prey selected at given round with a two-hybrid system. An "open reading frame", also referred to herein as

30

ORF, is a region of nucleic acid which encodes a polypeptide. This region may represent a portion of a coding sequence or a total sequence and be determined from a stop to stop codon or from a start to stop codon.

“DNA-binding domain” refers to a protein that specifically interacts with desoxyribonucleotide strands. A sequence-specific DNA binding protein binds to a specific sequence or family of specific sequences showing a high degree of sequence identity with each other.

The DNA binding domain of the bait polypeptide and the transcriptional activating domain of the prey polypeptide may be of different kinds. As an illustrative embodiment, these can be derived from LexA or also Gal4.

In one particular experiment of the yeast two-hybrid system, prey polypeptides are encoded by prey polynucleotides cloned in plasmid pACT11st carrying Leu2 selection gene transformed in Y187 yeast cells carrying leucine auxotrophy and bait polypeptide are encoded by bait polynucleotide cloned in plasmid pAS2ΔΔ carrying Trp1 selection gene transformed in CG1945 yeast cells carrying tryptophane auxotrophy.

In another aspect, the present invention relates to a bacterial two-hybrid system method for identifying a recombinant cell clone containing a prey polynucleotide encoding a prey polypeptide capable of interacting with a bait polypeptide comprising the steps of:

- a) transforming bacterial cell clones with a plasmid containing a bait polynucleotide encoding said bait polypeptide ;
 - b) rescuing prey plasmids containing prey polynucleotides from the collection according to the present invention ;
 - c) transforming the recombinant bacterial cell clones obtained in step a) with the plasmid rescued in step b) ;
 - d) cultivating bacterial recombinant cells obtained in step c) on selective medium ;
 - e) selecting recombinant cell clones capable of growing on selective medium.c)
- selecting recombinant cell clones capable of growing on selective medium.

In a preferred embodiment, the preparation of bacterial recombinant cells obtained in step c) of the bacterial two-hybrid system method for identifying a recombinant cell clone according to the invention comprises the following steps :

1) *E. coli* is firstly transformed with bait plamid (standard protocol with chimio- or electro-competent cells) ;

2) prey plasmids are rescued from collection according to the invention (prey plasmids are in *E. coli* bacterial strain, cf. protocol 1.B « the plasmid DNA
5 contained in *E. coli* are extracted (Qiagen) from aloquoted *E. coli* frozen cells ») ;

3) rescued prey plasmids are then transformed in recombinant *E. coli* of step 1 according to standard protocols of transformation (for example using electro- of chimio-competent cells).

In a particular embodiment, the invention is directed to a bacterial two-hybrid
10 system method for identifying a prey polynucleotide encoding a prey polypeptide capable of interacting with a bait polypeptide comprising the steps of :

- a) identifying a recombinant cell clone containing a prey polynucleotide encoding a prey polypeptide capable of interacting with a bait polypeptide according to the invention ; and
- 15 b) characterizing the prey polynucleotide contained in each recombinant cell clone selected in step a).

By bacterial two-hybrid system is intended a method that usually makes use of at least one reporter gene, the transcription of which is activated when a prey polypeptide and a bait polypeptide produced by recombinant cell, due to the triggering of the
20 transcription of said at least one reporter gene when both the specific domain contained in one prey polypeptide and the complementary domain contained in the bait polypeptide are in proximity one to the other.

In a particular embodiment of the bacterial two-hybrid system, specific domain of prey polypeptide and complementary domain of bait polypeptide are part of the
25 catalytic domain of an enzyme. Interaction of prey polypeptide and bait polypeptide allows restoration of enzyme catalytic domain and, as a consequence, to the restoration of the enzyme activity.

In a more preferred embodiment of the bacterial two-hybrid method, enzyme is *Bordetella pertussis* adenylate cyclase which activation, via proximity of T25 and T18
30 fragments of the catabolic domain, leads to cAMP synthesis, cAMP then triggers transcriptional activation of catabolic operons, such as lactose or maltose.

Still another aspect, the present invention relates to a method according to the invention, wherein the bait polypeptide and the prey polypeptide (encoded by a polynucleotide inserted in cell clone from the collection according to the present invention) are originating from the same prokaryotic micro-organism, particularly from
5 *Helicobacter pylori*, *Escherichia coli*, *Staphylococcus aureus* or *Streptococcus pneumoniae* or wherein the bait polypeptide is originating from a human polypeptide and the prey polypeptide is originating from a prokaryotic micro-organism, particularly from *Helicobacter pylori*.

Yet another aspect, the present invention relates to a recombinant diploid yeast
10 cell obtained by step a) of the yeast two-hybrid system method for identifying a recombinant cell clone according to the invention as described above.

The recombinant diploid yeast cell obtained by the the yeast two-hybrid system method for identifying a recombinant cell clone according to the invention, also forms part of the present invention.

15 By performing yeast or bacterial two-hybrid system, it can be possible to identify for one particular bait interacting prey polypeptide. Prey polynucleotide that has been selected by testing the collection in a screening two-hybrid method encodes for polypeptide interacting with a protein of interest.

The running of the two-hybrid method leads to the identification of interactions
20 between prokaryotic- prokaryotic polypeptides, especially *Helicobacter pylori*, *Escherichia coli*, *Staphylococcus aureus* or *Streptococcus pneumoniae* polypeptides, or eukaryotic-prokaryotic polypeptides, these interactions are also part of the invention.

In another aspect, the present invention is directed to a polynucleotide, or fragment thereof, encoding a prey polypeptide capable of interacting with a bait
25 polypeptide wherein said polynucleotide is identified by a method according to the invention.

In a preferred embodiment, the invention comprises the polynucleotides according to the invention, selected from the group consisting of:

a) a polynucleotide having the nucleic acid sequence of an ORF identified by the
30 reference indicated in the right column "interacting ORF" in table I, and fragment thereof having at least 12 consecutive nucleotides ;

- b) a polynucleotide having at least 80 %, preferably at least 85 %, 90 %, 95 % and 99 %, nucleotides identity degree after alignment to a nucleic acid sequence of a polynucleotide of a) ;
- c) a polynucleotide comprising the nucleic acid sequence of a polynucleotide of a) or b).

Still another aspect, the present invention is directed to a polynucleotide, or fragment thereof, encoding a bait polypeptide capable of interacting with a prey polypeptide wherein the polynucleotide encoding said prey polypeptide is identified by a method according to the invention.

In a preferred embodiment, the invention comprises the polynucleotides according to the invention, selected from the group consisting of :

- a) a polynucleotide having the nucleic acid sequence of an ORF identified by the reference indicated in the left column "bait polypeptide" in table I, and fragment thereof having at least 12 consecutive nucleotides ;
- b) a polynucleotide having at least 80 %, preferably at least 85 %, 90 %, 95 % and 99 %, identity degree after alignment to a nucleic acid sequence of a polynucleotide of a) ;
- c) a polynucleotide comprising the nucleic acid sequence of a polynucleotide of a) or b).

Yet another aspect, the present invention relates to a set of two polynucleotides consisting of a first polynucleotide, or fragment thereof, encoding a prey polypeptide capable of interacting with a bait polypeptide according to the invention and a second polynucleotide, or a fragment thereof having at least 12 consecutive nucleotides, encoding said bait polypeptide.

The polypeptides encoded by the polynucleotides according to the invention and the sets of two polypeptides encoded by the sets of two polynucleotides according to the invention, also form part of the invention.

In a preferred embodiment, the invention concerns an isolated complex comprising at least the two polypeptides encoded by a set of two polynucleotides according to the invention, preferably said two polypeptides are associated in the complex by affinity binding.

In a preferred embodiment, the invention concerns an isolated complex comprising at least a polypeptide encoded by the ORF HP1198 (or a fragment thereof, preferably one of its SID® domains, or homologous polypeptide thereof exhibiting at least 80 % identity degree) and a polypeptide encoded by the ORF HP1293 (or a fragment thereof, preferably one of its SID® domains, or homologous polypeptide thereof exhibiting at least 80 % identity degree).

In a preferred embodiment, the invention concerns an isolated complex comprising at least a polypeptide encoded by the ORF HP1198 (or a fragment thereof, preferably one of its SID® domains, or homologous polypeptide thereof exhibiting at least 80 % identity degree) and a polypeptide encoded by the ORF HP0088 (or a fragment thereof, preferably one of its SID® domains, or homologous polypeptide thereof exhibiting at least 80 % identity degree).

In a preferred embodiment, the invention concerns an isolated complex comprising at least a polypeptide encoded by the ORF HP1198 (or a fragment thereof, preferably one of its SID® domains, or homologous polypeptide thereof exhibiting at least 80 % identity degree) and a polypeptide encoded by the ORF HP1032 (or a fragment thereof, preferably one of its SID® domains, or homologous polypeptide thereof exhibiting at least 80 % identity degree).

In another aspect, the present invention relates to a protein-protein interaction wherein the two interacting proteins consist of a set of two polypeptides according to the invention.

In a preferred embodiment, the invention relates to the protein-protein interactions according to the invention, wherein the sets of two polypeptides consist of two *Helicobacter pylori*, *Escherichia coli*, *Staphylococcus aureus* or *Streptococcus pneumoniae* polypeptides.

When several reiterations of the two-hybrid method are performed and thus common bait and prey polypeptide are selected, a map of all the interactions between these polypeptides may be designed, that take into account of the known and/or suspected biological function of each of the interacting polypeptides.

Such an Proteins Interaction Map (PIM®) may help the one skilled in the art to decipher a whole metabolical and/or physiological pathway that is functionally active

within the host organism from which the initial DNA library is derived. Protein Interaction Map and computable version of PIM® are part of the present invention.

Therefore still another aspect, the present invention is directed to a computable readable medium (such as floppy disk, diskette, CD-rom, and all electronic or magnetic
5 format which can be read by a computer) having stored thereon protein-protein interactions according to the invention, preferably stored in a form of a protein interaction map, as showed, for example, in Fromont-Racine et al., Nature Genetics, 1997, Letter, 277-281, figure 3, page 279.

In a preferred embodiment, the invention comprises a computable readable
10 medium according to the invention, wherein the protein-protein interactions stored thereon are linked to annotated database, for example through Internet.

In an other preferred embodiment, the invention comprises a data bank containing the protein-protein interactions stored thereon, said databank being available on a World-Wide Web site, said databank may be annotated by means of others databank.

15 As the source genomic DNA is randomly fragmented before being inserted in recombinant vectors, several prey polypeptides may be selected for one bait polypeptide. Therefore it is possible to define the Selected Interacting Domain (SID®) which contains the precise polypeptide domain involved in the interaction between the prey polypeptide and the bait polypeptide.

20 So, in another aspect, the invention relates to a method for identifying a polynucleotide encoding a selected interacting domain (SID®) of a prey polypeptide of interest from a prokaryotic micro-organism capable of interacting with a bait polypeptide comprising the steps of :

- 25 a) selecting from prey polynucleotides identifying by a method according to the invention all prey polynucleotides encoding a polypeptide capable of interacting with said bait polypeptide and containing a nucleic acid fragment identical to a nucleic fragment of the polynucleotide encoding the prey polypeptide of interest ;
- b) determining the polynucleotide common to said all prey polynucleotides selected in step a); and
- 30 c) identifying the polynucleotide determining in step b) as being the polynucleotide encoding the selected interacting domain (SID®) of said prey polypeptide of interest.

The polynucleotides encoding a selected interacting domain (SID®) of a prey polypeptide of interest from a prokaryotic micro-organism capable of interacting with a bait polypeptide obtainable by this method, also form part of the invention.

In a particular embodiment, the prey polypeptide of interest is originating from
5 *Helicobacter pylori*, *Escherichia coli*, *Staphylococcus aureus* or *Streptococcus pneumoniae*.

In a preferred embodiment, the polynucleotides encoding a selected interacting domain (SID®) of a prey polypeptide of interest according to the invention are selected from the group consisting of :

- 10 a) a polynucleotide encoding an amino acids sequence identified by the reference indicated in the right column "SID®" in table II ;
- b) a polynucleotide having the sequence identified by the reference indicated in the right column "SID®" in table III ;
- c) fragment having at least 12, 15, 25 or 50 consecutive nucleotides of polynucleotide
15 of a) or b), complement thereof, and RNA corresponding to said polynucleotide ; and
- d) a polynucleotide having at least 80 %, preferably 85 %, 90 %, 95 % and 99 %, identity degree after alignment to a nucleic acid sequence of a polynucleotide of a) or b).

The term "complement thereof" are used herein to refer to the sequences of
20 polynucleotides which is capable of forming Watson & Crick base pairing with another specified polynucleotide throughout the entirety of the complementary region. This term is applied to pairs of polynucleotides based solely upon their sequences and not any particular set of conditions under which the two polynucleotides would actually bind.

The term "degree of sequence identity" is used herein to refer to comparisons
25 among polynucleotides and polypeptides, and are determined by comparing two optimally aligned sequences over a comparison window, wherein the portion of the polynucleotide or polypeptide sequence in the comparison window may comprise additions or deletions (i.e., gaps) as compared to the reference sequence (which does not comprise additions or deletions) for optimal alignment of the two sequences. The
30 percentage is calculated by determining the number of positions at which the identical nucleic acid base or amino acid residue occurs in both sequences to yield the number of matched positions, dividing the number of matched positions by the total number of

positions in the window of comparison and multiplying the result by 100 to yield the percentage of sequence identity. Homology is evaluated using any of the variety of sequence comparison algorithms and programs known in the art. Such algorithms and programs include, but are by no means limited to BLASTN, BLASTP (Altschul et al., 5 1990, J. Mol. Biol. 215(3): 403-410 / Altschul et al., 1993, Nature Genetics 3:266-272 / Altschul et al., 1997, Nuc. Acids Res. 25:3389-3402).

The definition of sequence identity given above is the definition that would use one of skill in the art. The definition by itself does not need the help of any algorithm, said algorithms being helpful only to achieve the optimal alignments of sequences, 10 rather than the calculation of sequence identity.

From the definition given above, it follows that there is a well defined and only one value for the sequence identity between two compared sequences which value corresponds to the value obtained for the best or optimal alignment.

In the BLAST N or BLAST P "BLAST 2 sequence" (Tatusova et al., *Blast 2 sequences - a new tool for comparing protein and nucleotide sequences*, FEMS Microbiol. Lett. 174 : 247-250) software which is available in the web site <http://www.ncbi.nlm.nih.gov/gorf/bl2.html>, and habitually used by the inventors and in general by the skilled man for comparing and determining the identity between two sequences, the "open gap penaltie" and « extension gap penaltie » parameters which 20 depend on the substitution matrix selected regarding the nature and the length of the sequence to be compared are directly selected by the software (i.e "5" and "2" respectively for substitution matrix BLOSUM-62). The identity percentage between the two sequences to be compared is directly calculated by the software.

In another object, the invention also comprises the polypeptides selected from 25 the group consisting of:

- a) a polypeptide having an amino acids sequence identified by the reference indicated in the right column "SID®" in table II, and fragment thereof having at least 5 consecutive amino acids ; and
- b) a polypeptide encoded by a polynucleotide encoding a selected interacting domain 30 (SID®) of a prey polypeptide of interest according to the invention.

Still another aspect, the invention relates to the use of a polynucleotide according to the present invention as a primer or a probe for the amplification and/or the

detection of polynucleotide encoded a prey polypeptide of interest, or its SID®, capable of interacting with a bait polypeptide according to the present invention.

In another aspect, the present invention concerns cloning or expression vector containing a polynucleotide according to the invention.

5 Particularly preferred vectors of the invention include the plasmid pACT11st, pAS2ΔΔ, pP6 or the plasmid selected from the group consisting of pT25, pKT25, pUT18 and pUT18C.

Further preferred vectors are self replicated or viral vectors, such as adenovirus, AAV, a retrovirus, a poxvirus or an herpes virus.

10 The vectors according to the invention, characterized in that they comprise the elements allowing the expression and/or the secretion of the said sequences in a host cell, also form part of the invention.

Vector according to the invention including elements allowing expression and/or secretion of said polynucleotide in a host cell also form part of the invention.

15 The vectors according to the invention characterized in that they comprise a promoter and/or regulator sequence, or a sequence for cellular addressing according to the invention, or one of their fragments, are also included in the invention.

The said vectors will preferably comprise a promoter, signals for initiation and termination of translation, as well as appropriate regions for regulation of transcription.

20 They may also be capable of being stably maintained in the cell and may optionally possess particular signals specifying the secretion of the translated protein.

These different control signals are chosen according to the cellular host used. To this end, the nucleic acid sequences according to the invention may be inserted into autonomously replicating vectors inside the chosen host, or integrative vectors of the
25 chosen host.

Among the autonomously or self replicating systems, there will be preferably used according to the host cell, systems of the plasmid or viral type, it being possible for the viral vectors to be in particular adenoviruses (Perricaudet et al., 1992, La Recherche
23 : 471-473, 1992), retroviruses, poxviruses or herpes viruses (Epstein et al., 1992, Médecine/Sciences 8 : 902-911, 1992). Persons skilled in the art know the technologies
30 which can be used for each of these systems.

When the integration of the sequence into the chromosomes of the host cell is desired, it will be possible to use, for example, systems of the plasmid or viral type ; such viruses will be, for example, retroviruses (Temin, 1986, In Kucherlapati R., ed. Gene Transfer, New York, Plenum Press, 149-187, 1986), or AAVs (Carter, 1993, *Curr. Op. Biotechnology* 3 : 533-539, 1993).

Such vectors will be prepared according to the methods commonly used by persons skilled in the art, and the clones resulting therefrom may be introduced into an appropriate host by standard methods such as, for example, lipofection, electroporation or heat shock.

The invention comprises, in addition, the host cells, in particular eukaryotic and prokaryotic cells, transformed by the vectors according to the invention.

Among the cells which can be used for these purposes, there may of course be mentioned bacterial cells (Olins et al., *Curr. Op. Biotechnology* 4 : 520-525, 1993), but also yeast cells (Buckholz, *Curr. Op. Biotechnology* 4 : 538-542, 1993), as well as animal cells, in particular mammalian cell cultures (Edwards and Aruffo, *Curr. Op. Biotechnology* 4 : 558-563, 1993), and in particular Chinese hamster ovary cells (CHO), but also insect cells in which it is possible to use methods using baculoviruses, for example (Luckow et al., *Curr. Op. Biotechnology* 4 : 564-572, 1993). A preferred cellular host for the expression of the proteins of the invention consists of the CHO cells.

The cells according to the invention can be used in a method for the production of a polypeptide according to the invention, as described below, and can also serve as a model for analysis and screening.

So, the present invention comprises a method for producing a polypeptide of the invention comprising the steps of :

- a) cultivating a host cell according to the invention under conditions and in culture medium allowing the growth of said host cell and the expression of said polypeptide ; and
- b) recovering said polypeptide directly from the culture medium or from said cultivated cell obtained in step a).

Recombinant polypeptide obtained by the method above also form part of the invention.

The term "recombinant polypeptide" is used herein to refer to polypeptides that have been artificially designed and which comprise at least two polypeptide sequences that are not found as contiguous polypeptide sequences in their initial natural environment, or to refer to polypeptides which have been expressed from a recombinant polynucleotide.

The method for the production of a polypeptide of the invention in recombinant form is itself included in the present invention, and is characterized in that the transformed cells, are cultured under conditions allowing the expression of a recombinant polypeptide encoded by a polynucleotide according to the invention, and in that the said recombinant polypeptide is recovered.

Also forming part of the invention is a method for the production of a heterologous polypeptide, characterized in that it uses a vector or a host cell according to the invention.

The recombinant polypeptides, characterized in that they are obtainable by the said method of production, also form part of the invention.

The recombinant polypeptides obtained as indicated above may be both in glycosylated and non-glycosylated form and may or may not have the natural tertiary structure.

These polypeptides may be produced from the polynucleotide, according to techniques for the production of recombinant polypeptides known to persons skilled in the art. In this case, the polynucleotide used is placed under the control of signals allowing its expression in a cellular host.

An effective system of production of a recombinant polypeptide requires having a vector and a host cell according to the invention.

These cells may be obtained by introducing into the host cells a nucleotide sequence inserted into a vector as defined above, and then culturing the said cells under conditions allowing the replication and/or expression of the transfected nucleotide sequence.

The methods for the purification of a recombinant polypeptide which are used are known to persons skilled in the art. The recombinant polypeptide may be purified from cell lysates and extracts, from the culture medium supernatant, by methods used individually or in combination, such as fractionation, chromatographic methods,

immunoaffinity techniques with the aid of specific mono- or polyclonal antibodies, and the like.

A preferred variant consists in producing a recombinant polypeptide fused with a "carrier" protein (chimeric protein). The advantage of this system is that it allows a
5 stabilization and a reduction in proteolysis of the recombinant product, an increase in solubility during in vitro renaturation and/or simplification of the purification when the fusion partner has affinity for a specific ligand.

The invention also relates to the synthesis of synthetic polypeptides of the invention, in particular by chemical synthesis.

10 The polypeptides according to the present invention can be obtained by chemical synthesis using any of the numerous known peptide syntheses, for example the techniques using solid phases or techniques using partial solid phases, by condensation of fragments or by a conventional synthesis in solution.

Also forming part of the invention are the methods for the determination of the
15 presence of a polynucleotide or a polypeptide encoded by involved in an protein-protein interaction of the present invention, characterized in that they use a polynucleotide or an antibody according to the invention.

These methods relate to, for example, the methods for the diagnosis *in vitro* of the presence in a biological sample of the procaryotic micro-organism from which said
20 polypeptide is originating. The polynucleotide analysed may be either the genomic DNA, the cDNA or the mRNA.

These methods can use the probes and primers of the present invention.

The term "primer" denotes a specific oligonucleotide sequence which is complementary to a target nucleotide sequence and used to hybridize to the target
25 nucleotide sequence. A primer serves as an initiation point for nucleotide polymerization catalyzed by either DNA polymerase, RNA polymerase or reverse transcriptase.

The term "probe" denotes a defined nucleic acid segment (or nucleotide analog segment, e.g., polynucleotide as defined hereinbelow) which can be used to identify a
30 specific polynucleotide sequence present in samples, said nucleic acid segment comprising a nucleotide sequence complementary of the specific polynucleotide sequence to be identified.

They are generally purified nucleic sequences for hybridization comprising at least 12 nucleotides, preferably at least 15, 20 and 25 nucleotides, characterized in that they can hybridize specifically with the polynucleotide chosen encoding the polypeptide of interest involved in an protein-protein interaction of the present invention.

5 Among the methods for the determination of the presence of a polynucleotide encoding a polypeptide of interest involved in an protein-protein interaction of the present invention, the methods comprising at least one stage for the so-called PCR (polymerase chain reaction) or PCR-like amplification of the target polynucleotide according to the invention with the aid of a pair of primers of nucleotide sequences
10 according to the invention are preferred.

PCR-like will be understood to mean all methods using direct or indirect reproductions of nucleic acid sequences, or alternatively in which the labelling systems have been amplified, these techniques are of course known, in general they involve the amplification of DNA by a polymerase; when the original sample is an RNA, it is
15 advisable to carry out a reverse transcription beforehand. There are currently a great number of methods allowing this amplification, for example the so-called NASBA "Nucleic Acid Sequence Based Amplification" (Compton J. 1991 Nature. 350 (6313): 91-92), TAS "Transcription based Amplification System" (Guatelli et al., 1990, Proc. Natl. Acad. Sci. USA. 35: 273-286), LCR "Ligase Chain Reaction" (Landegren et al.,
20 1998, Genome Research, 8:769-776), "Endo Run Amplification" (ERA), "Cycling Probe Reaction" (CPR), and SDA "Strand Displacement Amplification" (Walker et al., Nucleic Acids Res. 20: 1691-1696, 1992), methods well known to persons skilled in the art.

The invention comprises, in addition, methods for the determination of the
25 presence of a polypeptide of interest involved in an protein-protein interaction of the present invention, characterized in that an antibody according to the invention is brought into contact with the biological material to be tested, under conditions allowing the possible formation of specific immunological complexes between the said polypeptide and the said antibody, and in that the immuno-logical complexes possibly
30 formed are detected, such as, for example, methods using RIA or ELISA.

The transformed cells as described above can also be used as models so as to study the interactions between a polypeptide of the invention and their interacting

partners polypeptide, or between a polypeptide of the invention and chemical or protein compounds which are capable of modulating the protein-protein interaction according to the invention wherein said polypeptide of the invention is involved.

In particular, they may be used for the selection of products which interact with
5 a polypeptide of the invention, or one of its SID® domains, as cofactor or as inhibitor, in particular a competitive inhibitor, or alternatively having an agonist or antagonist activity on the protein-protein interaction wherein said polypeptide of the invention is involved. Preferably, the said transformed cells will be used as a model allowing, in particular, the selection of products which make it possible to prevent and/or to treat
10 pathologies induced by prokaryotic micro-organism.

Still another aspect of the invention pertains to a method for selecting an agent or compound capable of modulating the protein-protein interaction of a set of two polypeptides according to the invention comprising the steps of:

a) cultivating a recombinant cell clone containing a reporter gene expression of which
15 is toxic for said recombinant cell clone and transformed with two plasmids wherein :

i) the first plasmid contains a nucleic construct comprising a nucleic sequence encoding a first hybrid polypeptide containing one of said two polypeptides and a DNA binding domain ;

ii) the second plasmid contains a nucleic construct comprising a nucleic
20 sequence encoding a second hybrid polypeptide containing the second of said two polypeptides and an activating domain capable of activating said toxic reporter gene when the first and the second hybrid polypeptides are interacting ;

on a selective medium containing the agent to be tested and allowing the growth of said recombinant cell clone when the toxic reporter gene is not activated ; and

b) selecting agent which is capable of inhibiting the growth of the recombinant cell
25 clone cultivated in step a).

The invention also comprises a method for selecting an agent or compound capable of modulating the protein-protein interaction of a set of two polypeptides according to the invention comprising the steps of:

a) cultivating a recombinant cell clone, preferably permeable, containing a reporter
30 gene expression of which is toxic for said recombinant cell clone and transformed with two plasmids wherein :

i) the first plasmid contains a nucleic construct comprising a nucleic sequence encoding a first hybrid polypeptide containing one of said two polypeptides and the first domain of an enzyme ;

5 ii) the second plasmid contains a nucleic construct comprising a nucleic sequence encoding a second hybrid polypeptide containing the second of said two polypeptides and the second part of said enzyme capable of activating said toxic reporter gene when the first and the second hybrid polypeptides are interacting, said interaction restoring the activity of the enzyme ;

10 on a selective medium containing the agent to be tested and allowing the growth of said recombinant cell clone when the toxic reporter gene is not activated ; and

b) selecting agent which is capable of inhibiting the growth of the recombinant cell clone cultivated in step a).

In a preferred embodiment, said toxic reporter gene that can be used for negative selection, is URA3, CYH1 or CYH2 gene.

15 Still another aspect of the invention pertains to a method for selecting an agent or compound capable of modulating the protein-protein interaction of a set of two polypeptides according to the invention comprising the steps of :

20 a) cultivating a recombinant cell clone containing a reporter gene expression of which stimulates the growth of said recombinant cell clone and transformed with two plasmids wherein :

i) the first plasmid contains a nucleic construct comprising a nucleic sequence encoding a first hybrid polypeptide containing one of said two polypeptides and a DNA binding domain ;

25 ii) the second plasmid contains a nucleic construct comprising a nucleic sequence encoding a second hybrid polypeptide containing the second of said two polypeptides and an activating domain capable of activating said stimulating reporter gene when the first and the second hybrid polypeptides are interacting ;

on a selective medium containing the agent to be tested and allowing the normal growth of said recombinant cell clone when the stimulating reporter gene is not activated ; and

30 b) selecting agent which is capable of stimulating the growth of the recombinant cell clone cultivated in step a).

In a preferred embodiment, the method according to the invention for selecting an agent or compound capable of modulating the protein-protein interaction of a set of two polypeptides is a method for selecting an agent capable of modulating the interaction between a polypeptide encoded by the ORF HP1198 (or a fragment thereof, preferably one of its SID® domains, or homologous polypeptide thereof exhibiting at least 80 % identity degree) and a polypeptide encoded by the ORF HP1293 (or a fragment thereof, preferably one of its SID® domains, or homologous polypeptide thereof exhibiting at least 80 % identity degree).

In a preferred embodiment, the method according to the invention for selecting an agent or compound capable of modulating the protein-protein interaction of a set of two polypeptides is a method for selecting an agent capable of modulating the interaction between a polypeptide encoded by the ORF HP1198 (or a fragment thereof, preferably one of its SID® domains, or homologous polypeptide thereof exhibiting at least 80 % identity degree) and a polypeptide encoded by the ORF HP0088 (or a fragment thereof, preferably one of its SID® domains, or homologous polypeptide thereof exhibiting at least 80 % identity degree).

In a preferred embodiment, the method according to the invention for selecting an agent or compound capable of modulating the protein-protein interaction of a set of two polypeptides is a method for selecting an agent capable of modulating the interaction between a polypeptide encoded by the ORF HP1198 (or a fragment thereof, preferably one of its SID® domains, or homologous polypeptide thereof exhibiting at least 80 % identity degree) and a polypeptide encoded by the ORF HP1032 (or a fragment thereof, preferably one of its SID® domains, or homologous polypeptide thereof exhibiting at least 80 % identity degree).

In another embodiment of the invention, inventors provide a kit for screening a modulator agent comprising at least one recombinant diploid clone or a cell clone, haploid or diploid, transformed with a plasmid containing a sequence coding for a bait polypeptide and a plasmid containing the nucleotide sequence of a SID® or of a homologue polypeptide of SID®, said plasmids may be chosen between pACTIIst and pAS2ΔΔ.

SID® or homologue sequence of SID® acting on the same pair of interacting proteins may be also modulator agents.

Modulator agent selected by anyone of the yeast or bacterial two-hybrid system method of the invention also forms part of the invention.

These modulator agents of protein-protein interaction according to the invention may be obtained for example from a library of compounds.

5 Consequently, is also part of the invention a modulator agent selected by the method of the invention previously described capable of interfering with a protein-protein interaction according to the invention. This agent may modulate an interaction of the invention between two prokaryotic polypeptides, particularly between two *Helicobacter pylori*, *Escherichia coli*, *Staphylococcus aureus* or *Streptococcus*
10 *pneumoniae* polypeptides, or between a prokaryotic polypeptide, such as *Helicobacter pylori*, *Staphylococcus aureus* or *Streptococcus pneumoniae* polypeptide, and a polypeptide originating from a host organism of said prokaryotic micro-organism, such as mammal, particularly human.

These methods allow the selection of chemical or biochemical compound
15 capable of interacting, directly or indirectly, with the polynucleotide or the polypeptide encoded by of the invention, in particular capable of modulating the protein-protein interaction wherein said polypeptide of the invention is involved.

More particularly, the invention concerns modulator agent capable of modulating, more preferred of inhibiting, the viability and/or the growth of the
20 prokaryotic micro-organism, preferably *Helicobacter pylori*, *Staphylococcus aureus* or *Streptococcus pneumoniae*, from which is the protein-protein interaction.

For the screening of compounds capable of modulating the protein-protein interaction wherein said polypeptide of the invention is involved, the preferred principal effect is the effect of inhibiting the viability and/or the growth of the prokaryotic micro-
25 organism, preferably *Helicobacter pylori*, *Staphylococcus aureus* or *Streptococcus pneumoniae*, from which is the protein-protein interaction.

These effects of modulating the viability and/or the growth of prokaryotic micro-organisms can be analysed by any method known by a skilled man.

For example, a screening method of modulating agent can comprise the
30 following steps :

- Select one specific interaction.

- Transform a permeabilized yeast cell with plasmids containing bait polypeptide and prey polypeptide of the specific interaction.

- Plate a top agar containing transformed permeabilized yeast cells on square boxes (that already contains agarose gel).

5 - Apply by spotting the compounds to test on top agar as soon as it is solidified.

- Incubate, for example overnight at 30°C, and

- Analyse results : select lead compounds that prevent transformed permeabilized yeast cells from growing.

Screening may be used to test compounds capable of modifying the level and/or
10 the specificity of expression of the polynucleotide or the polypeptide encoded by of the invention involved in the protein-protein interaction according to the invention.

A quantitative or qualitative analysis of the expression of the gene encoded the polypeptide of the invention involved in the protein-protein interaction according to the invention can be carried out using primers or probes of the invention as DNA templates,
15 the term DNA templates designating nucleic acids having a sufficient length to allow a specific detection of the expression of mRNAs capable of hybridizing thereto. For example, the DNA templates contain nucleic acids derived from said gene, or sequences complementary thereto for which it is desired to estimate the level or the specificity of expression, and comprising at least 15, at least 25, at least 50, at least 100 or at least 500
20 consecutive nucleotides.

Another aspect of the present invention consists in methods of identifying molecules capable of binding to one of the set of two polypeptides of the invention involved in the protein-protein interaction. Such molecules can be used to modulate the viability and/or the growth of the prokaryotic micro-organism, preferably *Helicobacter*
25 *pylori*, from which is the protein-protein interaction activity. For example, such molecules can be used to stimulate or to inhibit a biological reaction involved in the viability and/or the growth of the prokaryotic micro-organism.

Numerous methods well known by the skilled man exist for identifying ligands for a defined polypeptide.

30 For example to identifying molecules capable of binding to one polypeptide of the set of two polypeptides of the invention involved in the protein-protein interaction, a subunit thereof or a fragment thereof comprising at least 10, at least 20, at least 30, or

more than 30 consecutive amino acids with small molecules such as those generated by combinatorial chemistry, it is possible to use an HPLC-coupled microdialysis, or an affinity capillary electrophoresis.

In other methods, the peptides or small molecules capable of interacting with said one of the set of two polypeptides of the invention, a subunit thereof or a fragment thereof may be linked to detectable markers such as radioactive, fluorescent or enzymatic markers. These labelled molecules are brought into contact with the immobilized said one of the set of two polypeptides of the invention, under conditions allowing a specific interaction. After elimination of the molecules which are not specifically bound, the bound molecules are detected by appropriate means.

In addition, the peptides or small molecules which bind to said one of the set of two polypeptides of the invention, preferably to its SID® binding site can be identified by competition experiments. In such experiments, said one of the set of two polypeptides of the invention, is immobilized on a surface. Increasing quantities of peptides or of small molecules are brought into contact with the immobilized said one of the set of two polypeptides of the invention in the presence of the second labelled polypeptide of said two polypeptides of the invention, designated labelled ligand. The labelled ligand may be labelled with a radioactive, fluorescent or enzymatic marker. The capacity of the molecule tested to interact with said one of the set of two polypeptides of the invention is determined by measuring the quantity of labelled ligand bound in the presence of the molecule tested. A decrease in the quantity of bound ligand when the molecule tested is present indicates that the latter is capable of interacting with said one of the set of two polypeptides of the invention.

The Biacore™ technology can also be used to carry out the screening of compounds capable of interacting with said one of the set of two polypeptides of the invention. This technology is described in Szabo et al. (1995) and in Edwards and Leartherbarrow (Analytical Biochemistry, 246, 1-6, 1997), of which the teaching is incorporated by reference, and makes it possible to detect interactions between molecules in real time without the use of labelling.

One of the main advantages of this method is that it allows the determination of the association constants between said one of the set of two polypeptides of the

invention and the interacting molecules. Thus, it is possible to specifically select the molecules interacting with high or low association constants.

The proteins or other molecules interacting said one of the set of two polypeptides of the invention can be identified using affinity columns which contain
5 said one of the set of two polypeptides of the invention. Said one of the set of two polypeptides of the invention may be attached to the column using conventional techniques including chemical coupling to an appropriate column matrix such as agarose, Affi Gel, or other matrices known to a person skilled in the art. In another aspect of the invention, the affinity column may contain chimeric proteins in which said
10 one of the set of two polypeptides of the invention would be fused, for example, with glutathione S-transferase. The molecules to be tested which are described above are then deposited on the column. The molecules interacting said one of the set of two polypeptides of the invention are retained by the column and can be isolated by elution.

The chemical or biochemical compounds, characterized in that they make it
15 possible to modulate, directly or indirectly, the protein-protein interaction according to the invention, and selected by the said methods defined above, also form part of the invention.

The use of a polypeptide according to the invention for the modulation of *Helicobacter pylori*'s protein interaction, also forms part of the present invention.

20 Still another aspect, the present invention is directed to a method for the production of monoclonal or polyclonal antibodies comprising the step of immunization of an animal or human organism with an immunogenic agent comprising a polypeptide, a vector according or a host cell according to the invention, and to antibodies obtained by said method.

25 The mono- or polyclonal antibodies or fragments thereof, chimeric or immuno-conjugated antibodies, characterized in that they are capable of specifically recognizing a polypeptide according to the invention, also form part of the invention.

As used herein, the term "antibody" refers to a polypeptide or group of polypeptides which are comprised of at least one binding domain, where an antibody
30 binding domain is formed from the folding of variable domains of an antibody molecule to form three-dimensional binding spaces with an internal surface shape and charge distribution complementary to the features of an antigenic determinant of an antigen,

which allows an immunological reaction with the antigen. Antibodies include recombinant proteins comprising the binding domains, as well as fragments, including Fab, Fab', F(ab)2, and F(ab')2 fragments.

Specific polyclonal antibodies may be obtained from a serum of an animal
5 immunized against a polypeptide according to the invention, in particular produced by genetic recombination or by peptide synthesis, according to the customary procedures, from a polynucleotide according to the invention.

The specific monoclonal antibodies may be obtained according to the conventional hybridoma culture method described by Kohler and Milstein (Kohler, G.
10 and Milstein, C., Nature 256:495, 1975).

The antibodies according to the invention are, for example, chimeric antibodies, humanized antibodies, Fab or F(ab')2 fragments. They may also be in the form of immunoconjugates or of labelled antibodies so as to obtain a detectable and/or quantifiable signal (Harlow, E., and D. Lane. 1988. Antibodies A Laboratory Manual.
15 Cold Spring Harbor Laboratory. pp. 53-242).

The invention also relates to methods for the detection and/or purification of a polypeptide according to the invention, characterized in that they use an antibody according to the invention.

The invention comprises, in addition, purified polypeptides, characterized in that
20 they are obtained by a method according to the invention.

Moreover, in addition to their use for the purification of polypeptides, the antibodies of the invention, in particular the monoclonal antibodies, may also be used for the detection of these polypeptides in a biological sample.

They thus constitute a means for the immunocytochemical or immuno-
25 histochemical analysis of the expression of polypeptide against which they are raised on specific tissue sections, for example by immunofluorescence, gold labelling, enzymatic immunoconjugates.

They make it possible in particular to detect expression of these polypeptides in the biological tissues or samples, which makes them useful for monitoring the progress
30 of a method of prevention or treatment.

More generally, the antibodies of the invention may be advantageously used in any situation where the expression of a polypeptide of the invention against which they are raised needs to be observed.

The invention finally relates to a polynucleotide, a polypeptide, a vector, a host cell, a modulator agent or an antibody to the invention as compound for the preparation of a medicament.

So the invention also encompasses a pharmaceutical composition comprising a compound selected from the group consisting of :

- a) a polynucleotide according to the invention ;
- 10 b) a polypeptide according to the invention ;
- c) a vector according to the invention ;
- d) a host cell according to the invention ;
- e) a modulator agent to the invention ; and
- f) an antibody to the invention.

15 A pharmaceutical composition according to the invention, wherein said composition is administered by any route such as intravenous route, intramuscular route, oral route, or mucosal route with an acceptable physiological carrier and/or adjuvant, also forms part of the invention.

The compounds according to the invention as a medicament for the prevention and/or treatment of pathologies of infection diseases induced by prokaryotic micro-organism are particularly preferred.

The most preferred are the compounds according to the invention, as a medicament for the prevention and/or treatment of infection diseases induced by *Helicobacter pylori*, *Staphylococcus aureus* or *Streptococcus pneumoniae*.

25 The compounds of the invention as active ingredients of a medicament will be preferably in soluble form, combined with a pharmaceutically acceptable vehicle.

Such compounds which can be used as a medicament offer a new approach for preventing and/or treating pathologies linked to infection by prokaryotic micro-organism such as *Helicobacter pylori*, *Staphylococcus aureus* or *Streptococcus pneumoniae*. Preferably, these compounds will be administered by the systemic route, in particular by the intravenous route, by the intramuscular or intradermal route or by the oral route.

Their modes of administration, optimum dosages and galenic forms can be determined according to the criteria generally taken into account in establishing a treatment suited to a patient, such as for example the age or body weight of the patient, the seriousness of his general condition, the tolerance to treatment and the side effects
5 observed, and the like.

The identified compounds can be administered to a mammal, including a human patient, alone or in pharmaceutical compositions where they are mixed with suitable carriers or excipient(s) at therapeutically effective doses to treat disorders associated with prokaryotic micro-organism infection. Techniques for formulation and
10 administration of the compounds of the instant application may be found in "Remington's Pharmaceutical Sciences", Mack Publishing Co., Easton, PA, latest edition.

Suitable routes of administration include oral, rectal, transmucosal, or intestinal administration, parenteral delivery, including intramuscular, subcutaneous, injections,
15 as well as intravenous, intraperitoneal or intranasal injections.

Pharmaceutical compositions and medicaments for use in accordance with the present invention may be formulated in a conventional manner using one or more physiologically acceptable carriers comprising excipients and auxiliaries. Proper formulation is dependent upon the route of administration chosen.

20 For injection, the agents of the invention may be formulated in aqueous solutions, preferably in physiologically compatible buffers such as Hanks's solution, Ringer's solution, or physiological saline buffer such as a phosphate or bicarbonate buffer. For transmucosal administration, penetrants appropriate to the barrier to be permeated are used in the formulation. Such penetrants are generally known in the art.

25 Pharmaceutical preparations which can be used orally include push-fit capsules made of gelatin, as well as soft, sealed capsules made of gelatin and a plasticizer, such as glycerol or sorbitol. The push-fit capsules can contain the active ingredients in admixture with fillers such as lactose, binders such as starches, and/or lubricants such as talc or magnesium stearate and, optionally, stabilizers. In soft capsules, the active
30 compounds may be dissolved or suspended in suitable liquids, such as fatty oils, liquid paraffin, or liquid polyethylene glycols. In addition, stabilizers may be added. All

formulations for oral administration should be in dosages suitable for such administration.

For buccal administration, the compositions may take the form of tablets or lozenges formulated in conventional manner.

5 For administration by inhalation, the compounds for use according to the present invention are conveniently delivered in the form of an aerosol spray presentation from pressurized packs or a nebulizer, with the use of a suitable gaseous propellant, e.g., carbon dioxide. In the case of a pressurized aerosol the dosage unit may be determined by providing a valve to deliver a metered amount. Capsules and cartridges of, e.g.,
10 gelatin, for use in an inhaler or insufflator, may be formulated containing a powder mix of the compound and a suitable powder base such as lactose or starch.

The compounds may be formulated for parenteral administration by injection, e.g., by bolus injection or continuous infusion. Formulations for injection may be presented in unit dosage form, e.g., in ampoules or in multi-dose containers, with an
15 added preservative. The compositions may take such forms as suspensions, solutions or emulsions in aqueous vehicles, and may contain formulatory agents such as suspending, stabilizing and/or dispersing agents.

Pharmaceutical formulations for parenteral administration include aqueous solutions of the active compounds in water-soluble form. Aqueous suspensions may
20 contain substances which increase the viscosity of the suspension, such as sodium carboxymethyl cellulose, sorbitol, or dextran. Optionally, the suspension may also contain suitable stabilizers or agents which increase the solubility of the compounds to allow for the preparation of highly concentrated solutions.

Alternatively, the active ingredient may be in powder or lyophilized form for
25 constitution with a suitable vehicle, such as sterile pyrogen-free water, before use.

Additionally, the compounds may be delivered using a sustained-release system, such as semipermeable matrices of solid hydrophobic polymers containing the therapeutic agent. Various sustained-release materials have been established and are well known by those skilled in the art. Sustained-release capsules may, depending on
30 their chemical nature, release the compounds for a few weeks up to over 100 days.

Depending on the chemical nature and the biological stability of the therapeutic reagent, additional strategies for protein stabilization may be employed.

The pharmaceutical compositions also may comprise suitable solid or gel phase carriers or excipients. Examples of such carriers or excipients include but are not limited to calcium carbonate, calcium phosphate, various sugars, starches, cellulose derivatives, gelatin, and polymers such as polyethylene glycols.

5 Pharmaceutical compositions suitable for use in the present invention include compositions wherein the active ingredients are contained in an effective amount to achieve their intended purpose. More specifically, a therapeutically effective amount means an amount effective to prevent development of or to alleviate the existing symptoms of the subject being treated. Determination of the effective amounts is well
10 within the capability of those skilled in the art, especially in light of the detailed disclosure provided herein.

For any compound used in the method of the invention, the therapeutically effective dose can be estimated initially from cell culture assays. For example, a dose can be formulated in animal models to achieve a circulating concentration range that
15 includes or encompasses a concentration point or range shown the desired effect in an in vitro system. Such information can be used to more accurately determine useful doses in humans.

A therapeutically effective dose refers to that amount of the compound that results in amelioration of symptoms in a patient. Toxicity and therapeutic efficacy of
20 such compounds can be determined by standard pharmaceutical procedures in cell cultures or experimental animals, e.g., for determining the LD50, (the dose lethal to 50 % of the test population) and the ED50 (the dose therapeutically effective in 50 % of the population). The dose ratio between toxic and therapeutic effects is the therapeutic index and it can be expressed as the ratio between LD50 and ED50. Compounds which
25 exhibit high therapeutic indices are preferred.

The data obtained from these cell culture assays and animal studies can be used in formulating a range of dosage for use in human. The dosage of such compounds lies preferably within a range of circulating concentrations that include the ED50, with little or no toxicity. The dosage may vary within this range depending upon the dosage form
30 employed and the route of administration utilized. The exact formulation, route of administration and dosage can be chosen by the individual physician in view of the

patient's condition (see, e.g., Fingl et al., 1975, in "The Pharmacological Basis of Therapeutics", Ch. 1).

Dosage amount and interval may be adjusted individually to provide plasma levels of the active compound which are sufficient to maintain the modulating effects.

5 Dosages necessary to achieve the modulating effect will depend on individual characteristics and route of administration.

The amount of composition administered will, of course, be dependent on the subject being treated, on the subject's weight, the severity of the affliction, the manner of administration and the judgment of the prescribing physician.

10 Other characteristics and advantages of the invention appear in the remainder of the description with the examples and figures whose legends are represented below.

Examples

Medium composition and standard protocols are available in Sambrook and
15 Maniatis (Sambrook, J., Fritsch, E.F., and T. Maniatis. (1989) Molecular Cloning: A Laboratory Manual. 2ed. Cold Spring Harbor Laboratory, Cold Spring Harbor, New York).

Example 1 : Preparation of a *Helicobacter pylori* genomic collection

1.A. Collection preparation and transformation in *Escherichia coli*

20 1.A.1. Fragmented of genomic DNA preparation

The *Helicobacter pylori* genomic DNA is fragmented in a nebulizer (GATC) for 1 minute, precipitated and resuspended in water.

The obtained nebulized genomic DNA is successively treated with Mung Bean Nuclease (Biolabs) (30 minutes at 30°C), T4 DNA polymerase (Biolabs) (10 minutes at
25 37°C) and Klenow enzyme (Pharmacia) (10 minutes at room temperature and 1 hour at 16°C).

DNA is then extracted, precipitated and resuspended in water.

1.A.2. Ligation of linkers to blunt-ended genomic DNA

Oligonucleotide PL160 (5' end phosphorylated) 1 µg/µl and PL159 2µg/µl.

30 Sequence of the oligo PL160 : 5'-ATCCCGGACGAAGGCC-3'.

Sequence of the oligo PL159 : 5'-GGCCTTCGTCCGG-3'.

Linkers were preincubated (5 minutes at 95°C, 10 minutes at 68°C, 15 minutes at 42°C) then cooled down at room temperature and ligated with genomic DNA inserts at 4°C overnight.

Linkers were further removed on a separation column (Chromaspin TE 400, Clontech), according to the manufacturer protocol.

1.A.3. Vector preparation

pACT11st is successively digest with BamHI restriction enzyme (Biolabs) for 1 hour at 37°C, dephosphorylated with Calf Intestine Phosphatase (CIP) (Biolabs) and filled in with dGTP using Vent DNA polymerase (exo-) (Biolabs), extracted, precipitated and resuspended in water.

1.A.4. Ligation between vector and insert of genomic DNA

The prepared vector is ligated overnight at 15°C with the genomic blunt ended DNA described in section 2 using T4 DNA ligase (Biolabs). The DNA is then precipitated and resuspended in water.

1.A.5. Library transformation in *Escherichia coli*

Transform DNA from section 1.A.4 into Electromax DH10B electrocompetent cells (Gibco BRL) with Cell Porator apparatus (Gibco BRL). Add 1 ml SOC medium and incubate transformed cells at 37°C for 1 hour. Add 9 ml volume of SOC medium per tube and plate on LB+ampicillin medium. Scrape colonies with liquid LB medium. Aliquot and freeze at -80°C.

The obtained collection of recombinant cell clones is named HGXBHP1 (CNCM No I-2181 deposited on April 13, 1999).

1.B. Collection transformation in *Saccharomyces cerevisiae*

The *Saccharomyces cerevisiae* strain (Y187 (MAT α Gal4 Δ Gal80 Δ ade2-101 His3 Leu2-3, -112 Trp1-901 Ura3-52 URA3::UASGAL1-LacZ Met)) transformed with the HGXBHP1 *H. pylori* genomic DNA library.

The plasmid DNA contained in *E. coli* are extracted (Qiagen) from aliquoted *E. coli* frozen cells (1.A.5.).

Grow *Saccharomyces cerevisiae* yeast Y187 in YPGlu.

Yeast transformation is performed according to standard protocol (Giest *et al.* Yeast, 11, 355-360, 1995) using yeast carrier DNA (Clontech). This experiment leads to

10^4 to 5.10^4 cells/ μ g DNA. Spread an estimating of 2.10^4 transformant on DO-Leu (Drop-out) medium per plates. Aliquot and freeze at -80°C .

1.C. Construction of bait plasmid

The genomic amplification of the ORF is obtained by PCR using the Pfu proofreading Taq polymerase (Stratagene) and 200 ng of genomic DNA as template.
5 PCR primers are chosen in regions flanking the ORF.

Set up the PCR program as followed :

	94°	45''	
	94°	45''	
10	48°	45''	x 30 cycles
	72°	6'	
	72°	10'	
	15°	∞	

Check amplification on agarose gel.

15 Purify PCR fragments with Qiaquick column (Qiagen) according to the manufacturer protocol.

Digest purified PCR fragments with adequate restriction enzymes.

Purify PCR fragments with Qiaquick column (Qiagen) according to the manufacturer protocol.

20 Ligate digested PCR fragments into an adequately digested and dephosphorylated bait vector (pAS2 $\Delta\Delta$) according to standard protocol (Maniatis *et al.*).

Transform into competent bacterial cells. Grow cells, extract DNA and sequence plasmid.

This protocole may also be applied to *E. coli*, *S. aureus* and *S. pneumoniae* genomic DNA.
25

Example 2 : Screening the collection with the two-hybrid in yeast system

2.A. The mating protocol

We have chosen the mating two-hybrid in yeast system (firstly described by Fromont Racine *et al.*, Nature Genetics, 1997, vol. 16, 277-282, Toward a functional
30 analysis of the yeast genome through exhaustive two-hybrid screens) for its advantages but we could also screen the *Helicobacter pylori* collection in classical two-hybrid system as described in Fields *et al.* or in a yeast reverse two-hybrid system.

The mating procedure allows a direct selection on selective plates because the two fusion proteins are already produced in the parental cells. No replica plating is required.

5 This protocol is written for the use of the library transformed into the Y187 strain.

Before mating, transform *S. cerevisiae* (CG 1945 strain (MATa Gal4-542 Gal180-538 ade2-101 His3*200 Leu2-3,-112 Trp1-901 Ura3-52 Lys2-801 URA3::GAL4 17mers (X3)-CyC1TATA-LacZ LYS2::GAL1UAS-GAL1TATA-HIS3 CYH^R)) according to step 1.B. and spread on DO-Trp medium.

10 Day 1, morning : preculture

Preculture of Y187 cells carrying the bait plasmid obtained at step 1.C. in 20 ml DO-Trp medium. Grow at 30°C with vigorous agitation.

Day 1, late afternoon : culture

15 Measure OD_{600nm} of the DO-Trp preculture of Y187 cells carrying the bait plasmid preculture.

Inoculate 150 ml DO-Trp at OD_{600nm} 0.006/ml, grow overnight at 30°C with vigorous agitation.

Day 2 : mating

medium and plates

20 5 YPGlu plates (Rich medium with glucose)

50 ml tube with 30 ml DO-Leu-Trp-His

100 ml flask with 20 ml of YPGlu

75 DO-Leu-Trp-His plates

2 DO-Leu plates

25 2 DO-Trp plates

2 DO-Leu-Trp plates

Measure OD_{600nm} of the DO-Trp culture. It should be around 1.

For the mating, you must use twice as many bait cells as library cells. To get a good mating efficiency, you must collect the cells at 10⁸ cells per cm².

30 Estimate the amount of bait culture (in ml) that makes up 80 OD_{600nm} units for the mating with the prokaryote library.

Thaw a vial containing the HGXYHP1 library slowly on ice. Add the contents of the vial to 20 ml YPGlu. Let those cells recover at 30°C, under gentle agitation for 10 minutes.

Mating

5 Put the 80 OD_{600nm} units of bait culture into a 250 ml flask.

Add the HGXYHP1 library culture to the bait culture. Transfer the mixture of diploids into 50 ml sterile tubes. Centrifuge, discard the supernatant and resuspend in YPGlu medium.

Distribute cells on YPGlu Plates (Rich medium with glucose).

10 Incubate plates cells-up at 30°C for 4h30min.

Collection of mated cells

Wash and rinse plates and spread collected cells on DO-Leu-Trp-His plates.

Day 4

15 Selection of clones capable of growing on DO-Leu-Trp-His : this medium allows us to isolate diploid clones presenting an interaction.

Count the His⁺ colonies on control plates.

The number of His⁺ cell clones will define which protocol is to be processed :

Upon 20.10⁶ His⁺ colonies :

- if number of His⁺ cell clones > 285 : then process overlay and then luminometry
- 20 protocols on blue colonies (2.B and 2.C) ;
- if number of His⁺ cell clones < 285 : process luminometry protocol (2.C).

The following step leads to the selection of the strongest interaction.

2.B. The X-Gal overlay assay

25 X-Gal overlay assay is performed directly on the selective medium plates after scoring the number of His⁺ colonies.

Material

Set up a waterbath. The water temperature should be 50°C.

- 0.5 M Na₂HPO₄ pH 7.5.
- 1.2 % Bacto-agar.
- 30 • 2 % X-Gal in DMF (dimethyl formamide).

- Overlay mixture : 0.25 M Na_2HPO_4 pH7.5, 0.5 % agar, 0.1 % SDS (Sodium dodecyl sulfate), 7 % DMF (LABOSI), 0.04 % X-Gal (ICN). For each plate, 10 ml overlay mixture are needed.
- DO-leu-trp-his plates.
- 5 • Sterile toothpicks.

Experiment

Temperature of the overlay mix should be between 45 and 50°C.

Pour the overlay-mix over the plates in portions of 10 ml.

Collect them when the top layer is settled.

- 10 Incubate plates overlay-up at 30°C. Note the time.

Check for blue colonies regularly. If no blue colony appears, wait for overnight incubation. Mark with a pen and number the positives.

Streak the positives colonies on fresh DO-Leu-Trp-His plates with a sterile toothpick.

15 2.C. The luminometry assay

- Grow His⁺ colonies overnight at 30°C in microtiter plates containing DO-Leu-Trp-His+Tetracyclin medium with shaking. The day after, dilute 15 times overnight culture into a new microtiter plate containing the same medium. Incubate 5 hours at 30°C with shaking. Dilute samples 5 times and read OD_{600nm}. Dilute again to obtain
- 20 between 10 000 and 75 000 yeast cells/well in 100 µl final volume.

Per well, add 76 µl of One Step Yeast Lysis Buffer (Tropix), 20 µl SapphireII Enhancer (Tropix), 4 µl Galacton Star (Tropix), incubate 40 minutes at 30°C.

Measure the β-Gal read-out (L) using a Luminometer (Trilux, Wallach).

Calculate value of OD_{600nm}/L and select interacting preys having highest values.

- 25 At this step of the protocol, we have isolated diploid cell clones presenting interaction. The next step is now to identify polypeptides involved in the selected interactions.

Example 3 : Identification of positive clones

30 3.A. PCR on yeast colonies

Introduction

PCR amplification of fragments of plasmid DNA directly on yeast colonies is a quick and efficient procedure to identify sequences cloned into this plasmid. It is directly derived from a published protocol (Wang H. et al., Analytical Biochemistry, 237, 145-146, 1996). However, it is not a standardized protocol : in our hands it varies from strain to strain, it is dependent of experimental conditions (number of cells, Taq polymerase source, etc). This protocol should be optimized to specific local conditions.

Materials

- For 1 well, PCR mix composition is :

- 10 32.5 µl water,
- 5 µl 10X PCR buffer (Pharmacia),
- 1 µl dNTP (10 mM each)
- 0.5 µl Taq polymerase (5u/µl) (Pharmacia),
- 0.5 µl oligonucleotide ABS1 10 pmole/µl: 5'-GCGTTTGAATCACTACAGG-3',
- 15 0.5 µl oligonucleotide ABS2 10 pmole/µl: 5'-CACGATGCACGTTGAAGTG-3'.
- 1 N NaOH.

Experiment

Grow positive colonies overnight at 30°C on a 96 well cell culture cluster (Costar), containing 150 µl DO-Leu-Trp-His+Tetracyclin with shaking. Resuspend culture and transfer immediately 100 µl on a Thermowell 96 (Costar).

Centrifuge 5 minutes at 4000 rpm at room temperature.

Remove supernatant.

Place the Thermowell in the thermocycler (GeneAmp 9700, Perkin Elmer) 5 minutes at 99.9°C and then 10 minutes at 4°C.

25 Add lysis buffer and incubate.

Centrifuge, transfer aliquot of supernatant in each well, add PCR mix, shake well.

Set up the PCR program as followed :

	94°C	3 minutes		x 35 cycles
30	94°C	30 secondes		
	53°C	1 minute 30 secondes		
	72°C	3 minutes		

72°C 5 minutes

15°C ∞

Check the quality, the quantity and the length of the PCR fragment on agarose gel.

- 5 The length of the cloned fragment is the estimated length of the PCR fragment minus 300 base pairs that correspond to the amplified flanking plasmid sequences.

3.B. Plasmids rescue from yeast by electroporation

Introduction

- 10 The previous protocol of PCR on yeast cell may not be successful, in such a case, we rescue plasmids from yeast by electroporation. This experiment allows the recovery of prey plasmids from yeast cells by transformation of *E. coli* with a yeast cellular extract. We can then amplify the prey plasmid and sequence the cloned fragment.

Material

- 15 Plasmid rescue

Glass beads 425-600 µm (Sigma)

Phenol/chloroform (1/1) premixed with isoamyl alcohol (Amresco)

Extraction buffer : 2 % Triton X100, 1 % SDS, 100 mM NaCl, 10 mM TrisHCl pH 8.0, 1 mM EDTA pH 8.0.

- 20 Mix ethanol/NH₄Ac : 6 volumes ethanol with 7.5 M NH₄ Acetate, 70 % Ethanol and yeast cells in patches on plates.

Electroporation

SOC medium

M9 medium

- 25 Selective plates : M9-Leu+Ampicillin

2 mm electroporation cuvettes (Eurogentech)

Experiment

Plasmid rescue

Prepare cell patch on DO-Leu-Trp-His with cell culture of section 2.C.

- 30 Scrape the cell of each patch in Eppendorf tube, add 300 µl of glass beads in each tube, then, add 200 µl extraction buffer and add 200 µl phenol:chloroform:isoamyl alcohol (25:24:1).

Centrifuge tubes 10 minutes at 15000 rpm.

Transfer 180 µl supernatant to a sterile Eppendorf tube and add to each 500 µl ethanol/NH₄Ac, vortex.

Centrifuge tubes 15 minutes, 15000 rpm at 4°C.

5 Wash pellet with 200 µl 70 % ethanol, remove ethanol and dry pellet.

Resuspend pellet in 10 µl water. Store extracts at -20°C.

Electroporation

Material : Electrocompetent MC1066 cells prepared according to standard protocols (Maniatis).

10 Add 1 µl of yeast plasmid DNA-extract to pre-chilled Eppendorf tube, and keep on ice.

Mix 1 µl plasmid yeast DNA-extract sample, add 20 µl electrocompetent cells and transfer in a cold electroporation cuvette.

Set the Biorad electroporator on 200 ohms resistance, 25 µF capacity ; 2.5
15 kVolts.

Place cuvette in the cuvette holder and electroporate.

Add 1 ml SOC into the cuvette and transfer the cell-mix into sterile Eppendorf tube.

Let cells recover for 30 minutes at 37°C, spin the cells down 1 minute, 4000x g
20 and pour off supernatant. Keep about 100 µl medium and use it to resuspend the cells and spread them on selective plates (e.g. M9-Leu plates).

Incubate plates for 36 hours at 37°C.

Grow one colony and extract plasmids. Check presence and size of insert through enzymatic digestion and agarose gel. Sequence insert.

25

Example 4 : Protein-Protein Interactions

For the purpose of this example, we have chosen to study *Helicobacter pylori*'s protein-protein interactions.

For each bait, the previous protocol leads to the identification of prey
30 polynucleotide sequences. In order to identify a protein-protein interaction, we need to characterize the obtained prey polypeptide sequence regarding the *Helicobacter pylori* genome.

This may be accomplished with a software program named blastwun (available on the Internet site of the University of Washington : <http://bioweb.pasteur.fr/seqanal/interfaces/blastwu.html>, this is a development version of software for gene and protein identification through similarity searches of protein and nucleotide sequence databases).

Blastwun program compares prey polypeptide insert sequence (rescued from prey plasmid) with whole *Helicobacter pylori* genome (available on N.C.B.I. web site : <http://www.ncbi.nlm.nih.gov> under GenBank accession number AE000511). This comparison leads to prey polynucleotide localizations in *H. pylori* genome, each localization having a score depending on the homology of sequence. For each prey polynucleotide, we consider the localization with the highest score and, if the insert sequence is included in and is in phase with an Open Reading Frame, we can identify one prey polypeptide interacting with one bait polypeptide.

Helicobacter pylori ORF's sequences are available on the World-Wide Web site of The Institute for Genomic Research (TIGR) at <http://www.tigr.org/tdb/mbd/hpdb/hpdb.html>.

This web page allows several requests concerning *Helicobacter pylori*'s genome, in particular, its ORF sequence. To get the sequences of a specific ORF, click on the window named « HP# » and click search. This operation leads to a new web page presenting nucleic and peptide sequence of the specific ORF.

Table I : protein interaction in *Helicobacter pylori* (see hereafter)

Example 5 : Identification of SID®

Experiment results in step 4. sequences of each prey fragment encoding for an interacting prey polypeptide.

By comparing and selecting the intersection of every isolated fragments that are included in the same polypeptide, we define the Selected Interacting Domain (SID®) see figure 7.

See results in Tables II and III.

Table I : Interaction involving polypeptides including *Helicobacter pylori* ORF

Bait polypeptides (ORF reference according to Tomb et al.)	Interacting ORF (ORF reference according to Tomb et al.)
HP0047	HP0047
HP0047	HP0048
HP0047	HP0695
HP0061	HP0066
HP0061	HP0978
HP0061	HP1409
HP0064	HP0063
HP0066	HP0066
HP0067	HP0069
HP0067	HP0609
HP0067	HP0768
HP0067	HP0770
HP0067	HP0956
HP0068	HP0070
HP0068	HP0118
HP0069	HP0067
HP0070	HP0068
HP0070	HP0070
HP0071	HP0278
HP0071	HP0417
HP0071	HP0570
HP0071	HP0775
HP0071	HP1340
HP0071	HP1409
HP0072	HP1489
HP0073	HP0073
HP0073	HP0232

HP0073	HP0259
HP0073	HP0067
HP0073	HP0232
HP0073	HP0705
HP0268	HP1198
HP0289	HP0289
HP0289	HP0289
HP0289	HP0887
HP0289	HP0922
HP0289	HP1038
HP0289	HP1543
HP0289	HP0289
HP0289	HP0289
HP0289	HP0610
HP0289	HP1355
HP0311	HP0312
HP0338	HP0132
HP0338	HP0337
HP0391	HP0099
HP0391	HP0392
HP0691	HP0692
HP0691	HP1362
HP0697	HP0012
HP0697	HP0048
HP0697	HP0558
HP0697	HP0599
HP0697	HP0696
HP0697	HP0864
HP0697	HP1037
HP0697	HP1038
HP0697	HP1299

HP0697	HP1576
HP0776	HP0067
HP0776	HP0278
HP0776	HP1378
HP0776	HP1409
HP0797	HP0289
HP0797	HP0887
HP0797	HP1349
HP0797	HP1377
HP0797	HP1409
HP0800	HP0433
HP0800	HP0687
HP0800	HP0800
HP0800	HP0801
HP0800	HP0924
HP0800	HP1267
HP0800	HP1460
HP0801	HP0152
HP0801	HP0800
HP0801	HP1513
HP0868	HP0088
HP0868	HP0327
HP0868	HP0869
HP0868	HP1142
HP0874	HP0875
HP0875	HP0874
HP0887	HP0459
HP0887	HP0610
HP0887	HP0699
HP0887	HP0887
HP0887	HP1157

HP0887	HP1460
HP0887	HP1464
HP0887	HP0610
HP0887	HP0887
HP0887	HP1157
HP0887	HP1464
HP0935	HP0072
HP0935	HP0528
HP0935	HP0657
HP0978	HP0979
HP0978	HP1583
HP1032	HP0643
HP1032	HP0818
HP1032	HP1122
HP1032	HP1198
HP1032	HP1316
HP1067	HP0392
HP1198	HP0088
HP1198	HP0268
HP1198	HP0293
HP1198	HP0452
HP1198	HP0705
HP1198	HP0775
HP1198	HP0965
HP1198	HP1032
HP1198	HP1114
HP1198	HP1124
HP1198	HP1198
HP1198	HP1274
HP1198	HP1378
HP1198	HP1411

HP1198	HP1541
HP1198	HP1032
HP1198	HP1218
HP1230	HP1230
HP1230	HP1529
HP1231	HP1247
HP1244	HP0857
HP1244	HP1246
HP1246	HP0121
HP1246	HP0326
HP1246	HP0407
HP1246	HP0886
HP1246	HP1035
HP1246	HP1244
HP1246	HP1460
HP1247	HP1231
HP1247	HP1353
HP1293	HP1198

* Tomb et al., 1997, Nature, 388, 539-547

As indicated page 547 in the document Tomb et al., the annotated *H. pylori* genome sequence and gene family alignments are available on the World-Wide Web site at <http://www.tigr.org/tdb/mbd/hpdb/hpdb.html>. For each ORF referenced HPXXXX, the detailed nucleic sequence, and amino acids sequence encoded by, can be obtained on the World-Wide Web site at <http://www.tigr.org/tdb/mbd/hpdb/hpdb.html>. by introducing said reference HPXXXX (see example 4).

Table II :

Bait polypeptides (ORF reference according to Tomb et al.)	SID® Amino Acid Sequence (SEQ ID N°)
HP0868	2
HP0868	4
HP0868	6
HP0868	8
HP0800	10
HP0800	12
HP0800	14
HP0800	16
HP0800	18
HP0800	20
HP0800	22
HP0801	24
HP0801	26
HP0801	28
HP0887	30
HP0887	32
HP0887	34
HP0887	36
HP0887	38
HP0887	40
HP0887	42
HP0289	44
HP0289	46
HP0289	48
HP0289	50
HP0289	52
HP0289	54

HP0289	56
HP0289	58
HP0289	60
HP0289	62
HP0068	64
HP0068	66
HP0047	68
HP0047	70
HP0047	72
HP0069	74
HP0066	76
HP0268	78
HP1293	80
HP0061	82
HP0061	84
HP0061	86
HP0064	88
HP1198	90
HP1198	92
HP1198	94
HP1198	96
HP1198	98
HP1198	100
HP1198	102
HP1198	104
HP1198	106
HP1198	108
HP1198	110
HP1198	112
HP1198	114
HP1198	116

HP1198	118
HP1231	120
HP1032	122
HP1032	124
HP1032	126
HP1032	128
HP1032	130
HP1230	132
HP1230	134
HP1529	136
HP0978	138
HP0978	140
HP0071	142
HP0071	144
HP0071	146
HP0071	148
HP0071	150
HP0071	152
HP0073	154
HP0073	156
HP0073	158
HP0935	160
HP0935	162
HP0935	164
HP0338	166
HP0338	168
HP1246	170
HP1246	172
HP1246	174
HP1246	176
HP1246	178

HP1246	180
HP1246	182
HP0797	184
HP0797	186
HP0797	188
HP0797	190
HP0797	192
HP0311	194
HP0067	196
HP0067	198
HP0067	200
HP0067	202
HP0067	204
HP1244	206
HP1244	208
HP1067	210
HP0875	212
HP0776	214
HP0776	216
HP0776	218
HP0776	220
HP0697	222
HP0697	224
HP0697	226
HP0697	228
HP0697	230
HP0697	232
HP0697	234
HP0697	236
HP0697	238
HP0697	240

HP0887	242
HP0887	244
HP0887	246
HP0887	248
HP1247	250
HP1247	252
HP0874	254
HP0072	256
HP0391	258
HP0391	260
HP0070	262
HP0070	264
HP0691	266
HP0691	268
HP1198	270
HP1198	272
HP0073	274
HP0073	276
HP0073	278

Table III :

Bait polypeptides (ORF reference according to Tomb et al.)	SID ® Nucleic acid sequence (SEQ ID N°)
HP0868	1
HP0868	3
HP0868	5
HP0868	7
HP0800	9
HP0800	11
HP0800	13
HP0800	15
HP0800	17
HP0800	19
HP0800	21
HP0801	23
HP0801	25
HP0801	27
HP0887	29
HP0887	31
HP0887	33
HP0887	35
HP0887	37
HP0887	39
HP0887	41
HP0289	43
HP0289	45
HP0289	47
HP0289	49
HP0289	51
HP0289	53

HP0289	55
HP0289	57
HP0289	59
HP0289	61
HP0068	63
HP0068	65
HP0047	67
HP0047	69
HP0047	71
HP0069	73
HP0066	75
HP0268	77
HP1293	79
HP0061	81
HP0061	83
HP0061	85
HP0064	87
HP1198	89
HP1198	91
HP1198	93
HP1198	95
HP1198	97
HP1198	99
HP1198	101
HP1198	103
HP1198	105
HP1198	107
HP1198	109
HP1198	111
HP1198	113
HP1198	115

HP1198	117
HP1231	119
HP1032	121
HP1032	123
HP1032	125
HP1032	127
HP1032	129
HP1230	131
HP1230	133
HP1529	135
HP0978	137
HP0978	139
HP0071	141
HP0071	143
HP0071	145
HP0071	147
HP0071	149
HP0071	151
HP0073	153
HP0073	155
HP0073	157
HP0935	159
HP0935	161
HP0935	163
HP0338	165
HP0338	167
HP1246	169
HP1246	171
HP1246	173
HP1246	175
HP1246	177

HP1246	179
HP1246	181
HP0797	183
HP0797	185
HP0797	187
HP0797	189
HP0797	191
HP0311	193
HP0067	195
HP0067	197
HP0067	199
HP0067	201
HP0067	203
HP1244	205
HP1244	207
HP1067	209
HP0875	211
HP0776	213
HP0776	215
HP0776	217
HP0776	219
HP0697	221
HP0697	223
HP0697	225
HP0697	227
HP0697	229
HP0697	231
HP0697	233
HP0697	235
HP0697	237
HP0697	239

HP0887	241
HP0887	243
HP0887	245
HP0887	247
HP1247	249
HP1247	251
HP0874	253
HP0072	255
HP0391	257
HP0391	259
HP0070	261
HP0070	263
HP0691	265
HP0691	267
HP1198	269
HP1198	271
HP0073	273
HP0073	275
HP0073	277

Claims

1. A method for producing a collection of recombinant cell clones usable for two-hybrid systems comprising the steps of :

- 5 a) fragmenting DNA ;
b) inserting polynucleotidic fragments obtained in step a) in plasmids in such a way that the expression of said plasmids in host cell leads to an hybrid polypeptide containing a specific domain capable of activating a reporter gene when associated with a complementary domain ;
10 c) transforming cell clones with plasmids obtained in step b) ; and
d) optionally, selecting the transformed recombinant cell clones obtained in step c) ;
wherein DNA of step a) is genomic DNA obtained from a prokaryotic micro-organism.

2. A method according to claim 1, wherein the step a) of fragmenting DNA is carried by a nebulization process.

- 15 3. A method according to claim 1 or 2, wherein the prokaryotic micro-organism is *Helicobacter pylori*.

4. A method according claim 1 or 2, wherein the prokaryotic micro-organism is *Staphylococcus aureus*.

5. A method according claim 1 or 2, wherein the prokaryotic micro-
20 organism is *Streptococcus pneumoniae*.

6. A method according claim 1 or 2, wherein the prokaryotic micro-organism is *Escherichia coli*.

7. Collection of recombinant cell clones usable for two-hybrid systems obtainable by a method according to anyone of claims 1 to 6.

- 25 8. Collection of recombinant cell clones usable for two-hybrid systems, each recombinant cell clone containing a polynucleotide inserted in a plasmid whose expression leads to hybrid polypeptide containing a specific domain, wherein the said polynucleotide is a genomic DNA fragment obtained from a prokaryotic micro-organism.

- 30 9. Collection of recombinant cell clones usable for two-hybrid systems according to claim 8 wherein said genomic DNA fragment is obtained by a fragmentation process by nebulization.

10. Collection of recombinant cell clones according to anyone of claims 7 to 9, wherein the prokaryotic micro-organism is *Helicobacter pylori*.

11. Collection of recombinant cell clones according to anyone of claims 7 to 9, wherein the prokaryotic micro-organism is *Staphylococcus aureus*.

5 12. Collection of recombinant cell clones according to anyone of claims 7 to 9, wherein the prokaryotic micro-organism is *Streptococcus pneumoniae*.

13. Collection of recombinant cell clones according to anyone of claims 7 to 9, wherein the prokaryotic micro-organism is *Escherichia coli*.

14. Collection of recombinant cell clones according to anyone of claims 7 to 10 13, wherein the recombinant cell clones are selected from the group consisting of Gram+ or Gram- bacteria, yeasts, fungi and mammalian cells.

15. Collection of recombinant cell clones according to claim 14, wherein the recombinant cell clones are selected from the group consisting of *Escherichia coli* bacteria and *Saccharomyces cerevisiae* yeast.

15 16. Collection of recombinant cell clones according to claim 15, wherein the recombinant cell clones are *E. coli* bacteria.

17. Collection of recombinant cell clones according to anyone of claims 7 to 16, wherein the plasmids comprise at least a nucleic sequence coding a promoter, a specific domain, a multicloning site where the said polypeptide is cloned, and a 20 selection marker.

18. Collection of recombinant cell clones according to anyone of claims 7 to 17, wherein the polynucleotide is inserted in the plasmid pACT11st or pP6.

19. Collection of recombinant cell clones according to claim 18, wherein the collection contains 10^6 to 10^7 recombinant *Escherichia coli* clones and wherein the 25 proportion of different cell clones with insert is at least 60 %.

20. Collection of recombinant cell clones according to claim 18 or 19 filed with CNCM on April 13, 1999 under number I-2181.

21. Collection of recombinant cell clones according to claim 18 or 19 filed with CNCM on March 23, 2000 under number I-2416.

30 22. Collection of recombinant cell clones according to claim 18 or 19 filed with CNCM on March 23, 2000 under number I-2414.

23. Collection of recombinant cell clones according to claim 18 or 19 filed with CNCM on March 23, 2000 under number I-2415.

24. Collection of recombinant cell clones according to claim 18 or 19 filed with CNCM on March 23, 2000 under number I-2417.

5 25. Collection of recombinant cell clones according to claim 18, wherein the collection contains 10^5 to 1.5×10^6 haploid recombinant *Saccharomyces cerevisiae* clones and wherein the proportion of different cell clones with insert is at least 60 %.

26. Collection of recombinant cell clones according to claim 18 or 25 filed with CNCM on April 13, 1999 under number I-2182.

10 27. Collection of recombinant cell clones according to claim 18 or 25 filed with CNCM on March 23, 2000 under number I-2420.

28. Collection of recombinant cell clones according to claim 18 or 25 filed with CNCM on March 23, 2000 under number I-2419.

15 29. Collection of recombinant cell clones according to claim 18 or 25 filed with CNCM on March 23, 2000 under number I-2418.

30. Collection of recombinant cell clones according to anyone of claims 7 to 17, wherein the polynucleotide is inserted in the plasmid pAS2 $\Delta\Delta$.

20 31. Collection of recombinant cell clones according to anyone of claims 7 to 17, wherein the polynucleotide is inserted in a plasmid selected from the group consisting of pT25, pKT25, pUT18 and pUT18C.

32. Kit for screening protein-protein interaction comprising a collection of recombinant cell clones usable for two-hybrid systems according to anyone of claims 7 to 31.

25 33. A yeast two-hybrid system method for identifying a recombinant cell clone containing a prey polynucleotide encoding a prey polypeptide capable of interacting with a bait polypeptide comprising the steps of:

a) mating at least one first haploid recombinant cell clone of a collection of recombinant cell clones according to claim 25 or 26 transformed with a plasmid containing the prey polynucleotide to be assayed with a second haploid recombinant

30 *S. cerevisiae* cell clone transformed with a plasmid containing a bait polynucleotide encoding said bait polypeptide ;

b) cultivating diploid cell obtained in step a) on selective medium ; and

c) selecting recombinant cell clones capable of growing on selective medium.

34. A yeast two-hybrid system method for identifying a prey polynucleotide encoding a prey polypeptide capable of interacting with a bait polypeptide comprising the steps of:

- 5 a) identifying a recombinant cell clone containing a prey polynucleotide encoding a prey polypeptide capable of interacting with a bait polypeptide according to claim 33 ; and
- b) characterizing the prey polynucleotide contained in each recombinant cell clone selected in step a).

10 35. A bacterial two-hybrid system method for identifying a recombinant cell clone containing a prey polynucleotide encoding a prey polypeptide capable of interacting with a bait polypeptide comprising the steps of:

- a) transforming bacterial cell clones with a plasmid containing a bait polynucleotide encoding said bait polypeptide ;
- 15 b) rescuing prey plasmids containing prey polynucleotides from the collection according to claims 7 to 31 ;
- c) transforming the recombinant bacterial cell clones obtained in step a) with the plasmid rescued in step b) ;
- d) cultivating bacterial recombinant cells obtained in step c) on selective medium ;
- 20 e) selecting recombinant cell clones capable of growing on selective medium.

36. A bacterial two-hybrid system method for identifying a prey polynucleotide encoding a prey polypeptide capable of interacting with a bait polypeptide comprising the steps of:

- 25 a) identifying a bacterial recombinant cell clone containing a prey polynucleotide encoding a prey polypeptide capable of interacting with a bait polypeptide according to claim 35 ; and
- b) characterizing the prey polynucleotide contained in each recombinant cell clone selected in step a).

37. Method according to anyone of claims 33 to 36, wherein the bait polypeptide is a human polypeptide.

38. Method according to anyone of claims 33 to 36, wherein the bait polypeptide is a *Helicobacter pylori* polypeptide.

39. Method according to anyone of claims 33 to 36, wherein the bait polypeptide is a *Staphylococcus aureus* polypeptide.

40. Method according to anyone of claims 33 to 36, wherein the bait polypeptide is a *Streptococcus pneumoniae* polypeptide.

5 41. Method according to anyone of claims 33 to 36, wherein the bait polypeptide is a *Escherichia coli* polypeptide.

42. A recombinant diploid yeast cell obtained by step a) of the method according to claim 33.

10 43. A recombinant diploid yeast cell obtained by the method according to claim 33.

44. A set of two purified or isolated polynucleotides consisting of a first polynucleotide, or fragment thereof, encoding a prey polypeptide capable of interacting with a bait polypeptide and a second polynucleotide, or a fragment thereof having at least 12 consecutive nucleotides, encoding said bait polypeptide wherein the prey polynucleotide is identified by a method according to anyone of claims 34 and 36.

15 45. A set of two purified or isolated polypeptides encoded by the set of two polynucleotides according to claim 44.

46. Protein-protein interaction wherein the two interacting proteins consist of a set of two polypeptides according to claim 45.

20 47. Protein-protein interaction according to claim 46, wherein the set of two polypeptides consists of two *Helicobacter pylori* polypeptides.

48. Protein-protein interaction according to claim 46, wherein the set of two polypeptides consists of two *Staphylococcus aureus* polypeptides.

25 49. Protein-protein interaction according to claim 46, wherein the set of two polypeptides consists of two *Streptococcus pneumoniae* polypeptides.

50. Protein-protein interaction according to claim 46, wherein the set of two polypeptides consists of two *Escherichia coli* polypeptides.

51. Isolated complex comprising at least the two polypeptides encoded by the set of two polynucleotides according to claim 44.

30 52. Isolated complex according to claim 51, characterized in that said complex comprises at least a polypeptide encoded by the ORF HP1198 and a polypeptide encoded by the ORF HP1293.

53. Isolated complex according to claim 51, characterized in that said complex comprises at least a polypeptide encoded by the ORF HP1198 and a polypeptide encoded by the ORF HP0088.

54. Isolated complex according to claim 51, characterized in that said
5 complex comprises at least a polypeptide encoded by the ORF HP1198 and a polypeptide encoded by the ORF HP1032.

55. A computable readable medium having stored thereon protein-protein interactions according to claim 46 to 50.

56. A computable readable medium according to claim 55, wherein the
10 protein-protein interactions stored thereon is stored in a form of a map.

57. A computable readable medium according to claim 55 or 56, wherein the protein-protein interactions stored thereon are linked to annotated database through Internet.

58. A method for identifying a polynucleotide encoding a selecting
15 interacting domain (SID®) of a prey polypeptide of interest from a prokaryotic micro-organism capable of interacting with a bait polypeptide comprising the steps of :

a) selecting from prey polynucleotides identified by a method according to claim 34 or
36 all prey polynucleotides encoding a polypeptide capable of interacting with said
bait polypeptide and containing a nucleic acid fragment identical to a nucleic
20 fragment of the polynucleotide encoding the prey polypeptide of interest ;

b) determining the polynucleotide common to said all prey polynucleotides selected in
step a) ; and

c) identifying the polynucleotide determining in step b) as being the polynucleotide
encoding the selected interacting domain (SID®) of said prey polypeptide of interest.

59. Purified or isolated polynucleotide encoding a selecting interacting
25 domain (SID®) of a prey polypeptide of interest from a prokaryotic micro-organism capable of interacting with a bait polypeptide obtainable by a method according to claim 58.

60. Purified or isolated polynucleotide according to claim 59 selected from
30 the group consisting of :

a) a polynucleotide encoding an amino acids sequence identified by the reference indicated in the right column "SID®" in table II ;

- b) a polynucleotide having the sequence identified by the reference indicated in the right column "SID®" in table III ;
- c) fragment having at least 12 consecutive nucleotides of polynucleotide of a) or b), complement thereof, and RNA corresponding to said polynucleotide ; and
- 5 d) a polynucleotide having at least 80 % identity degree after alignment to a nucleic acid sequence of a polynucleotide of a) or b).

61. Purified or isolated polypeptide selected from the group consisting of :

- a) a polypeptide having an amino acids sequence identified by the reference indicated in the right column "SID®" in table II, and fragment thereof having at least 5
- 10 consecutive amino acids ; and
- b) a polypeptide encoded by a polynucleotide according to claim 59 or 60.

62. Use of a polynucleotide according to claim 60 as a primer for amplification.

63. Use of a polynucleotide according to claim 60 as a specific probe for

15 detection.

64. Cloning or expression vector containing a polynucleotide according to anyone of claims 59 and 60.

65. Vector according to claim 64, wherein the vector is the plasmid pACTIIst, pAS2ΔΔ or pP6.

20 66. Vector according to claim 64, wherein the vector is the plasmid selected from the group consisting of pT25, pKT25, pUT18 and pUT18C.

67. Vector according to claim 64, wherein the vector is self replicated.

68. Vector according to claim 64 or 67, wherein the vector is a viral vector.

69. Vector according to claim 68, wherein the vector is chosen between an

25 adenovirus, AAV, a retrovirus, a proxivirus or an herpes virus.

70. Vector according to anyone of claims 64 to 69 including elements allowing expression and/or secretion of said polynucleotide in a host cell.

71. Host cell transformed with a vector according to anyone of claims 64 to

70.

30 72. Host cell according to claim 71, wherein the host cell is a prokaryotic cell.

73. Host cell according to claim 71, wherein the host cell is an eukaryotic cell.

74. Method for producing a polypeptide according to anyone of claims 45 and 61, comprising the steps of :

- 5 a) cultivating a host cell according to anyone of claims 71 to 73 under conditions and in culture medium allowing the growth of said host cell and the expression of said polypeptide; and
b) recovering said polypeptide directly from the culture medium or from said cultivated cell obtained in step a).

10 75. Purified or isolated polypeptide obtained by the method according to claim 74.

76. A method for selecting an agent capable of modulating the protein-protein interaction of a step of two polypeptides according to claim 45 comprising the steps of :

- 15 a) cultivating a recombinant cell clone containing a reporter gene expression of which is toxic for said recombinant cell clone and transformed with two plasmids wherein :
i) the first plasmid contains a nucleic construct comprising a nucleic sequence encoding a first hybrid polypeptide containing one of said two polypeptides and a DNA binding domain ;
20 ii) the second plasmid contains a nucleic construct comprising a nucleic sequence encoding a second hybrid polypeptide containing the second of said two polypeptides and an activating domain capable of activating said toxic reporter gene when the first and the second hybrid polypeptides are interacting ;

25 on a selective medium containing the agent to be tested and allowing the growth of said recombinant cell clone when the toxic reporter gene is not activated ; and

- b) selecting agent which is capable of inhibiting the growth of the recombinant cell clone cultivated in step a).

30 77. A method for selecting an agent capable of modulating the protein-protein interaction of a set of two polypeptides according to claim 45 comprising the steps of :

a) cultivating a permeable recombinant cell clone containing a reporter gene expression of which is toxic for said recombinant cell clone and transformed with two plasmids wherein :

- 5 i) the first plasmid contains a nucleic construct comprising a nucleic sequence encoding a first hybrid polypeptide containing one of said two polypeptides and the first domain of an enzyme ;
- ii) the second plasmid contains a nucleic construct comprising a nucleic sequence encoding a second hybrid polypeptide containing the second of said two polypeptides and the second part of said enzyme capable of activating said toxic reporter gene
- 10 when the first and the second hybrid polypeptides are interacting, said interaction restoring the activity of the enzyme ;

on a selective medium containing the agent to be tested and allowing the growth of said recombinant cell clone when the toxic reporter gene is not activated ; and

- b) selecting agent which is capable of inhibiting the growth of the recombinant cell clone cultivated in step a).
- 15

78. A method according to claim 77, for selecting an agent capable of modulating the interaction between a polypeptide encoded by the ORF HP1198, or a fragment or homologous polypeptide thereof, and a polypeptide encoded by the ORF HP1293, or a fragment or homologous polypeptide thereof.

- 20 79. A method according to claim 77, for selecting an agent capable of modulating the interaction between a polypeptide encoded by the ORF HP1198, or a fragment or homologous polypeptide thereof, and a polypeptide encoded by the ORF HP0088, or a fragment thereof or homologous polypeptide thereof.

80. A method according to claim 77, for selecting an agent capable of

25 modulating the interaction between a polypeptide encoded by the ORF HP1198, or a fragment or homologous polypeptide thereof, and a polypeptide encoded by the ORF HP1032, or a fragment or homologous polypeptide thereof.

81. Modulator agent selected by the method according to claim 76 or 77.

82. Kit for screening a modulator agent comprising at least one recombinant
- 30 transformed cell clone according to step a) of claim 76 or 77.

83. Use of a polypeptide according to anyone of claims 45 and 61 for the modulation of *Helicobacter pylori*'s protein interaction.

84. Method for the production of monoclonal or polyclonal comprising the step of immunization of an animal or human organism with an immunogenic agent comprising a polypeptide according to anyone of claims 45 and 61, a vector according to anyone of claims 65 to 70 or a host cell according to anyone of claims 71 to 73.

5 85. Antibody obtained by the method according to claim 84.

86. A pharmaceutical composition comprising a compound selected from the group consisting of:

- a) a polynucleotide according to anyone of claims 59 and 60 ;
- b) a polypeptide according to anyone of claims 45 and 61 ;
- 10 c) a vector according to anyone of claims 62 to 70 ;
- d) a host cell according to anyone of claims 71 to 73 ;
- e) a modulator agent according to claim 80 ; and
- f) an antibody according to claim 85.

87. A pharmaceutical composition according to claim 86, wherein said
15 composition is administered by any route such as intravenous route, intramuscular route, oral route, or mucosal route with an acceptable physiological carrier and/or adjuvant.

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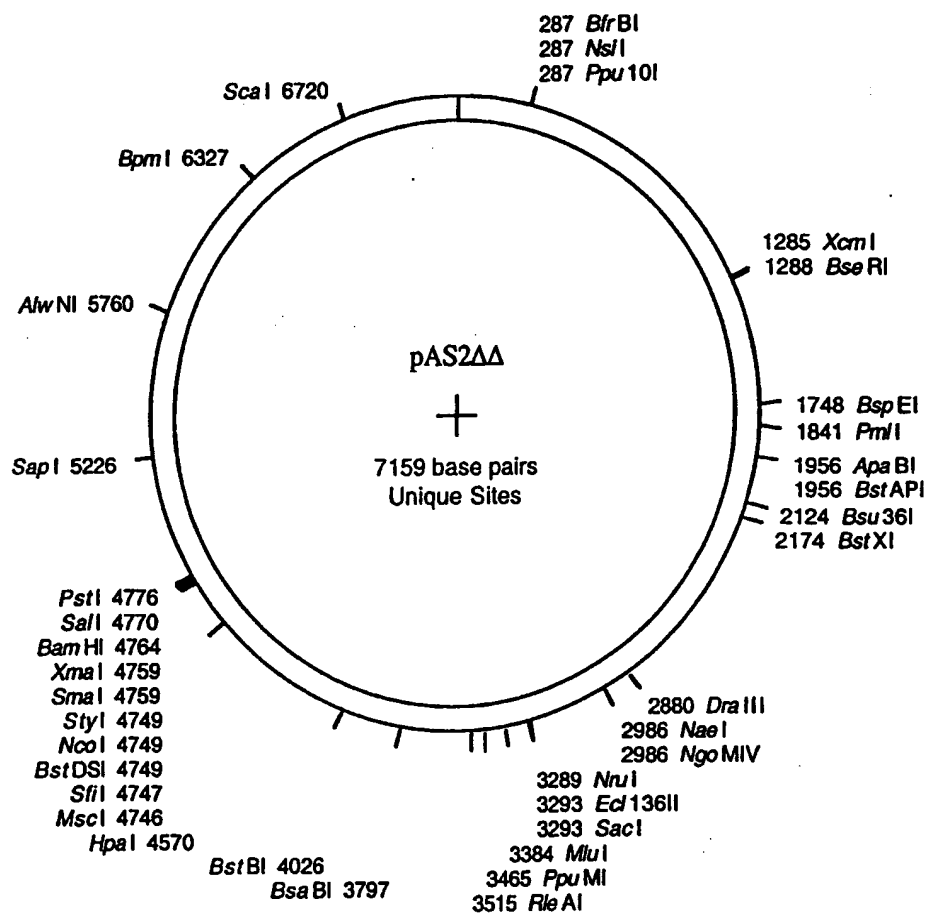


FIGURE 1

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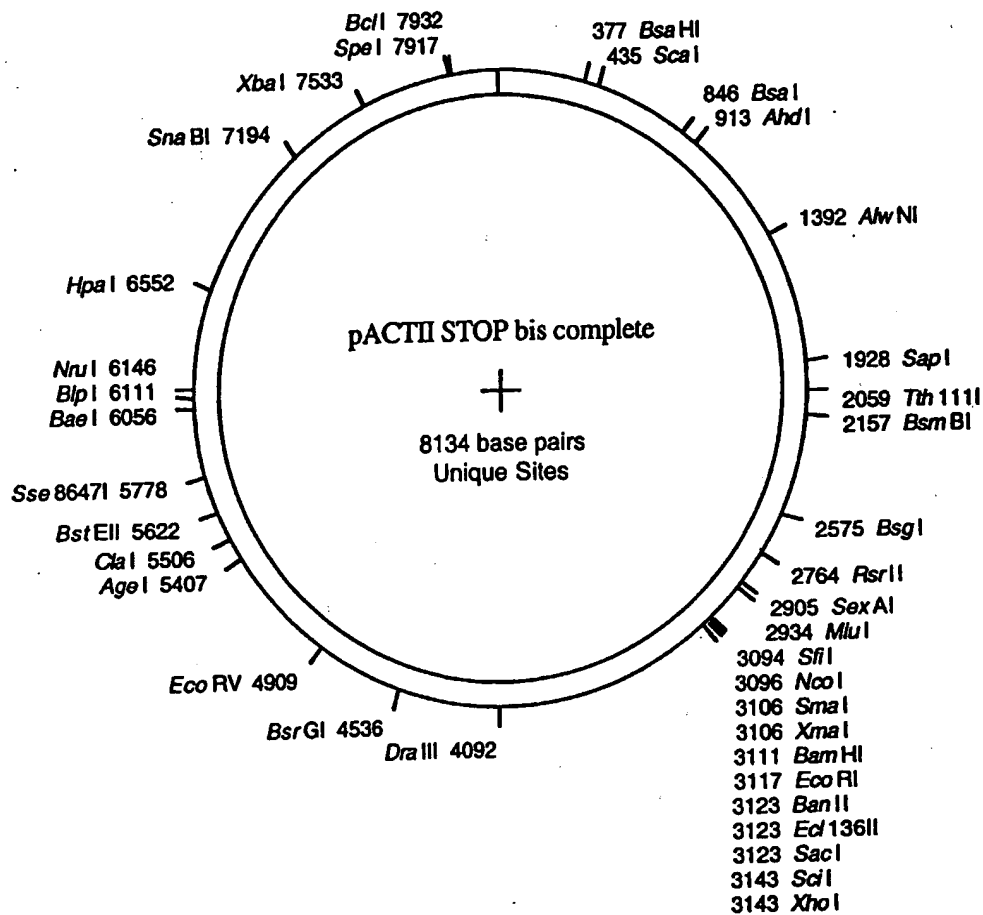


FIGURE 2

VECTORS TO CREATE FUSED PROTEINS WITH T18 FRAGMENT

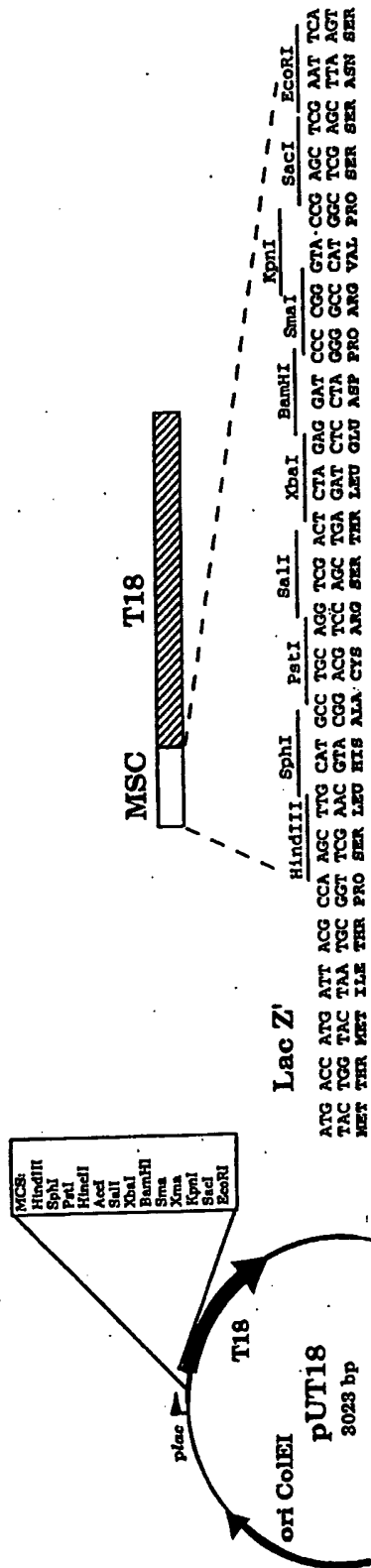


FIGURE 3

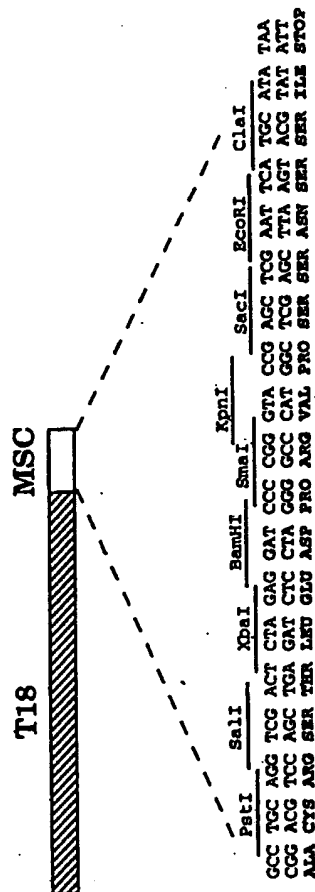
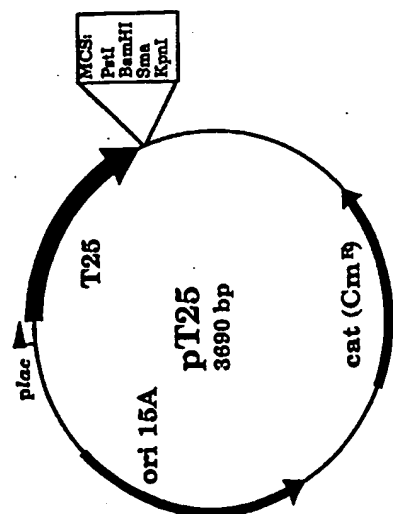


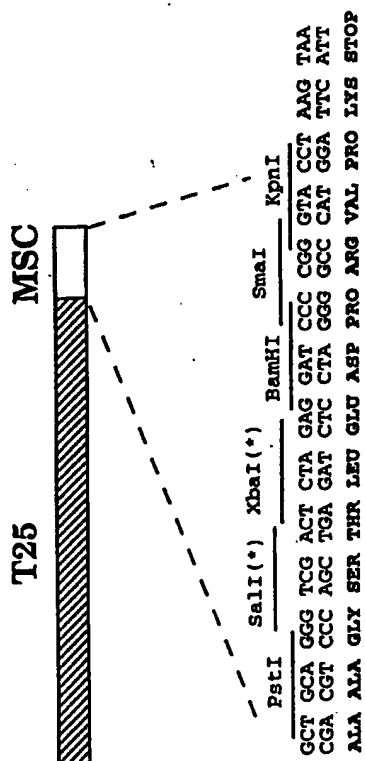
FIGURE 4

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VECTORS TO CREATE FUSED PROTEINS WITH T25 FRAGMENT

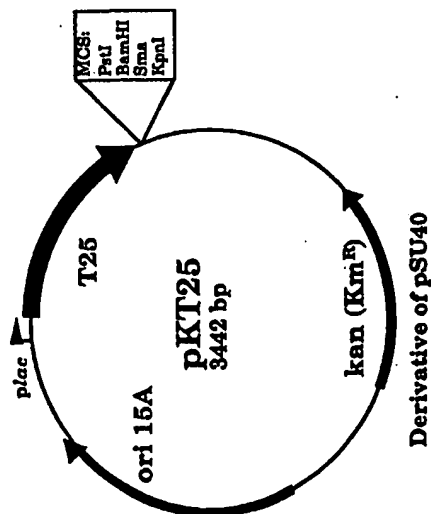


Derivative of pACYC184

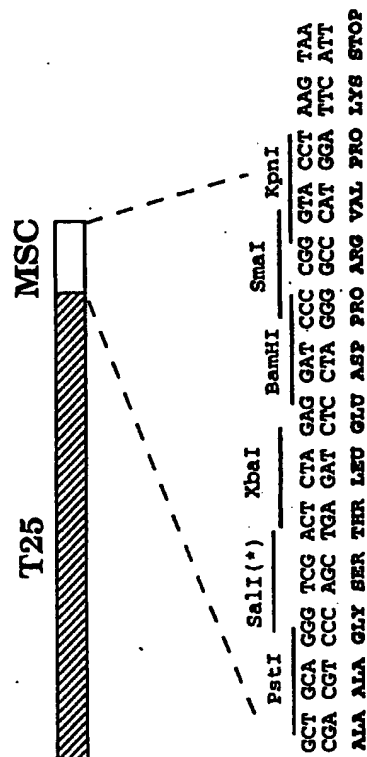


(*) Restriction sites are not unique

FIGURE 5



Derivative of pSU40



(*) Restriction site is not unique

FIGURE 6

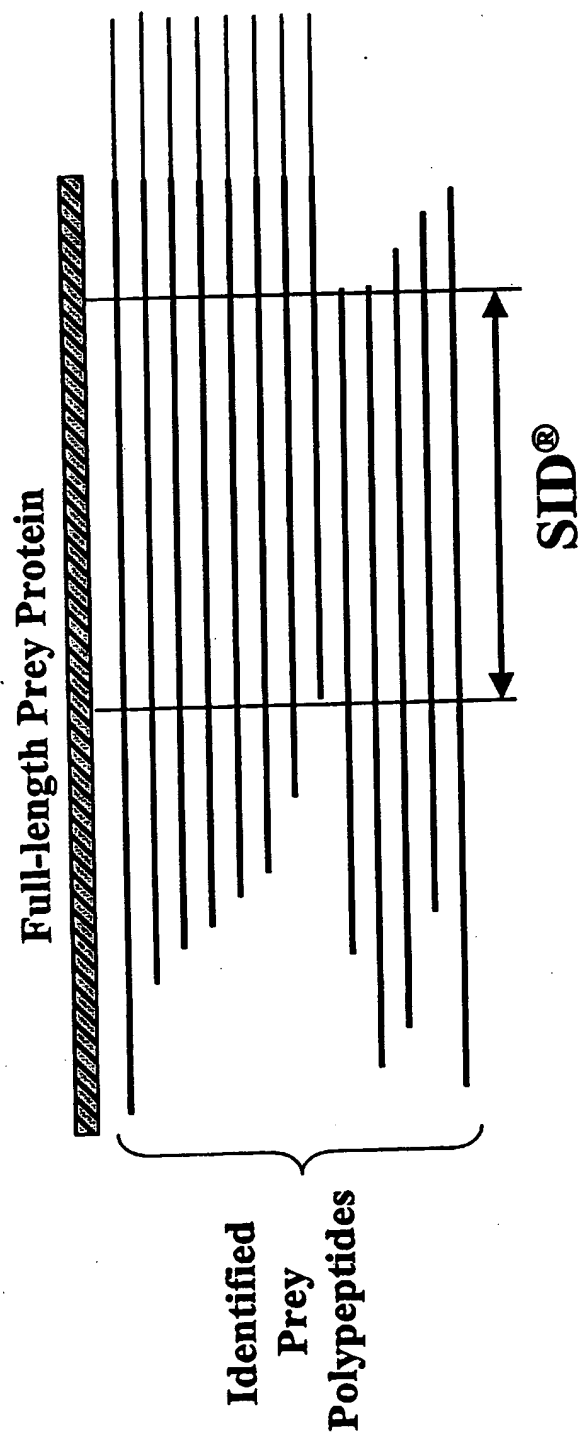


FIGURE 7

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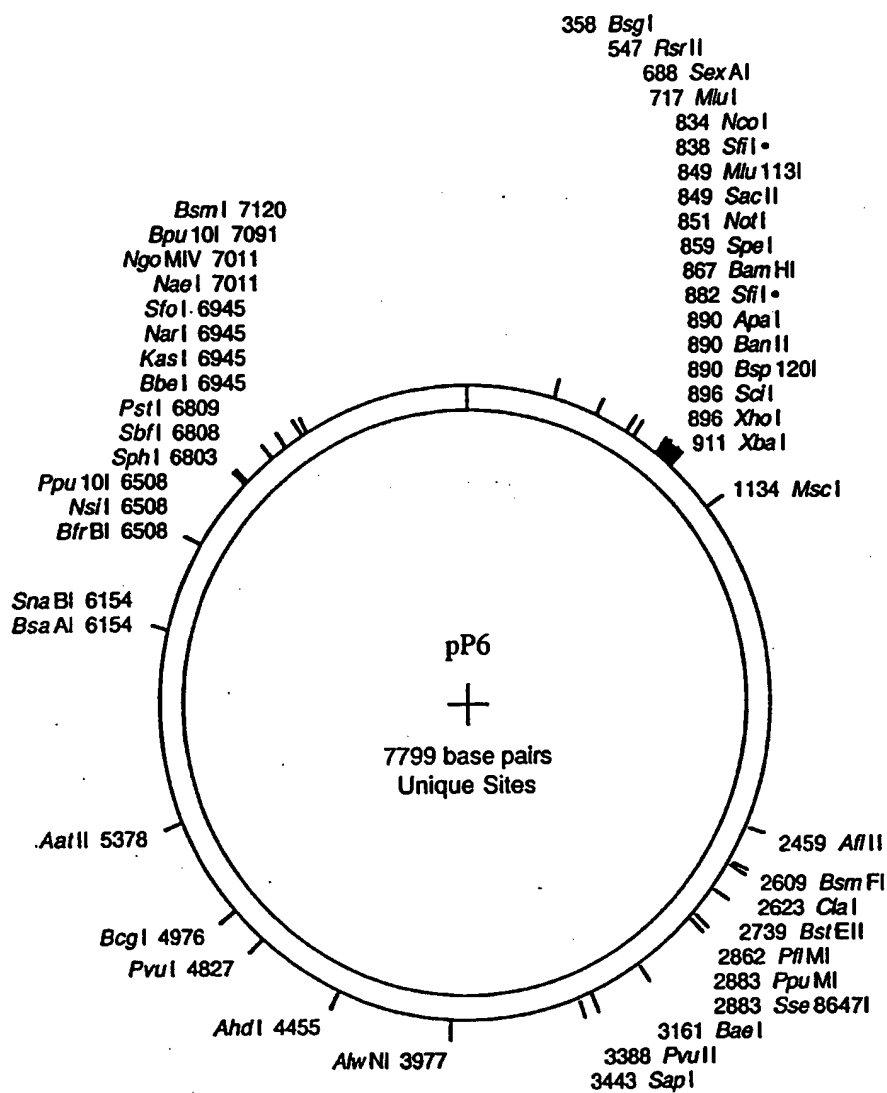


FIGURE 8

SEQUENCE LISTING

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<120> Collection of Prokaryotic DNA for Two-Hybrid System, Helicobacter pylori Protein-Protein Interactions and Applications thereof

<130> D18015

<140>

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<150> EP 99401066.8

<151> 1999-04-30

<160> 278

<170> PatentIn Ver. 2.1

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gct gaa gaa gtg ggg ctt tcg tta gat aaa gtg aag aat gtg att aag   96
Ala Glu Glu Val Gly Leu Ser Leu Asp Lys Val Lys Asn Val Ile Lys
      20           25           30
gtg act aaa gag cct atc agt ttg gaa acc cca gtc ggc aat gat gat   144
Val Thr Lys Glu Pro Ile Ser Leu Glu Thr Pro Val Gly Asn Asp Asp
      35           40           45
gat ggc aag ttt ggg gat ttc gtg gaa gat aag aat atc gtc agc tcc   192
Asp Gly Lys Phe Gly Asp Phe Val Glu Asp Lys Asn Ile Val Ser Ser
      50           55           60
att gat cac atc atg cga gaa gat ttg aaa gca caa att gaa agc gtt   240
Ile Asp His Ile Met Arg Glu Asp Leu Lys Ala Gln Ile Glu Ser Val
      65           70           75           80
ttg gat cag ttg aat gag cga gaa aaa gcg gtg atc cgc atg cgt ttt   288
Leu Asp Gln Leu Asn Glu Arg Glu Lys Ala Val Ile Arg Met Arg Phe
      85           90           95
ggg ctt tta gac gat gaa agc gat cga act tta gaa gaa att ggc aag   336
Gly Leu Leu Asp Glu Ser Asp Arg Thr Leu Glu Glu Ile Gly Lys
      100          105          110
gaa ttg aat gtt act aga gaa agg gtg cgc cag att gaa agc tct gcg   384
Glu Leu Asn Val Thr Arg Glu Arg Val Arg Gln Ile Glu Ser Ser Ala
      115          120          125
att aaa aaa ttg aga agc ccg cag tac ggg cgc att tta aga aac tat   432
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ttg cgc att
Leu Arg Ile
145

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<213> Helicobacter pylori

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      20           25           30
Val Thr Lys Glu Pro Ile Ser Leu Glu Thr Pro Val Gly Asn Asp Asp

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          35          40          45
Asp Gly Lys Phe Gly Asp Phe Val Glu Asp Lys Asn Ile Val Ser Ser
  50          55          60
Ile Asp His Ile Met Arg Glu Asp Leu Lys Ala Gln Ile Glu Ser Val
  65          70          75          80
Leu Asp Gln Leu Asn Glu Arg Glu Lys Ala Val Ile Arg Met Arg Phe
          85          90          95
Gly Leu Leu Asp Asp Glu Ser Asp Arg Thr Leu Glu Glu Ile Gly Lys
          100          105          110
Glu Leu Asn Val Thr Arg Glu Arg Val Arg Gln Ile Glu Ser Ser Ala
          115          120          125
Ile Lys Lys Leu Arg Ser Pro Gln Tyr Gly Arg Ile Leu Arg Asn Tyr
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gtt ggc tct atc act aaa atc aat ttt ttt cat aag cat ggg tat ttg 96
Val Gly Ser Ile Thr Lys Ile Asn Phe Phe His Lys His Gly Tyr Leu
          20          25          30
ggg att tat aaa aac cct ttt ttg aaa aat ggg gga gaa acg att tta 144
Gly Ile Tyr Lys Asn Pro Phe Leu Lys Asn Gly Gly Glu Thr Ile Leu
          35          40          45
aaa gcc ttg gaa ttt atc gct ttt gaa gag ttc caa tta cat tct ttg 192
Lys Ala Leu Glu Phe Ile Ala Phe Glu Glu Phe Gln Leu His Ser Leu
          50          55          60
cat tta gaa gtg atg gaa aac aat ttc aaa gcg atc gct ttt tat gaa 240
His Leu Glu Val Met Glu Asn Asn Phe Lys Ala Ile Ala Phe Tyr Glu
          65          70          75          80
aaa aac cat tat gag tta gag ggg cgt ttg aaa ggc ttt att tct aaa 288
Lys Asn His Tyr Glu Leu Glu Gly Arg Leu Lys Gly Phe Ile Ser Lys
          85          90          95
gat aag gag ttt ata gac gtt ctt ttg tat tat aag gat aag aaa gga 336
Asp Lys Glu Phe Ile Asp Val Leu Leu Tyr Tyr Lys Asp Lys Lys Gly
          100          105          110
tat aat gat caa tct ctt cta aaa ctt 363
Tyr Asn Asp Gln Ser Leu Leu Lys Leu
          115          120

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<210> 4

<211> 121

<212> PRT

<213> Helicobacter pylori

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          20          25          30
Gly Ile Tyr Lys Asn Pro Phe Leu Lys Asn Gly Gly Glu Thr Ile Leu
          35          40          45
Lys Ala Leu Glu Phe Ile Ala Phe Glu Glu Phe Gln Leu His Ser Leu
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Ala Glu

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1				5					10					15				
aag	att	gtt	gaa	aca	gaa	cag	aag	aat	caa	caa	act	aaa	ttg	gac	aca		96	
Lys	Ile	Val	Glu	Thr	Glu	Gln	Lys	Asn	Gln	Gln	Thr	Lys	Leu	Asp	Thr			
			20					25					30					
gaa	aat	ttg	aaa	ata	att	att	gaa	act	ttg	aga	agt	aaa	atc	aat	ggg		144	
Glu	Asn	Leu	Lys	Ile	Ile	Ile	Glu	Thr	Leu	Arg	Ser	Lys	Ile	Asn	Gly			
			35				40					45						
aat	cag	caa	aag	atg	ctt	gat	aaa	agt	aaa	gaa	atg	agc	aga	aat	ttt		192	
Asn	Gln	Gln	Lys	Met	Leu	Asp	Lys	Ser	Lys	Glu	Met	Ser	Arg	Asn	Phe			
			50			55						60						
aag	ctt	gat	agc	act	aaa	aac	gag	ata	gac	gca	att	aaa	gat	ttg	att		240	
Lys	Leu	Asp	Ser	Thr	Lys	Asn	Glu	Ile	Asp	Ala	Ile	Lys	Asp	Leu	Ile			
65				70					75					80				
aaa	aag	gct	aat	gag	caa	ata	gcc	aat	tat	aat	gag	atg	ata	aag	gat		288	
Lys	Lys	Ala	Asn	Glu	Gln	Ile	Ala	Asn	Tyr	Asn	Glu	Met	Ile	Lys	Asp			
				85				90						95				
att	gaa	aaa	cag	aaa	aag	agt	tgt	aag	gaa	caa	act	tgg	aaa	ttt	cta		336	

Ile Glu Lys Gln Lys Lys Ser Cys Lys Glu Gln Thr Trp Lys Phe Leu
 100 105 110
 gtc aat gaa ttt aaa agt gat ata caa gaa tat aat aaa aag tat tgc 384
 Val Asn Glu Phe Lys Ser Asp Ile Gln Glu Tyr Asn Lys Lys Tyr Cys
 115 120 125
 ggt ttg gag aaa gga ata aac aat tta gag aaa gca att agt gaa aat 432
 Gly Leu Glu Lys Gly Ile Asn Asn Leu Glu Lys Ala Ile Ser Glu Asn
 130 135 140
 caa gaa gag gta aag aaa tta gaa aat gaa 462
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 20 25 30
 Glu Asn Leu Lys Ile Ile Ile Glu Thr Leu Arg Ser Lys Ile Asn Gly
 35 40 45
 Asn Gln Gln Lys Met Leu Asp Lys Ser Lys Glu Met Ser Arg Asn Phe
 50 55 60
 Lys Leu Asp Ser Thr Lys Asn Glu Ile Asp Ala Ile Lys Asp Leu Ile
 65 70 75 80
 Lys Lys Ala Asn Glu Gln Ile Ala Asn Tyr Asn Glu Met Ile Lys Asp
 85 90 95
 Ile Glu Lys Gln Lys Lys Ser Cys Lys Glu Gln Thr Trp Lys Phe Leu
 100 105 110
 Val Asn Glu Phe Lys Ser Asp Ile Gln Glu Tyr Asn Lys Lys Tyr Cys
 115 120 125
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 130 135 140
 Gln Glu Glu Val Lys Lys Leu Glu Asn Glu
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 ttg caa gtg tta gaa tgt gaa aat tgt tca atg act tat tat gat aga 96
 Leu Gln Val Leu Glu Cys Glu Asn Cys Ser Met Thr Tyr Tyr Asp Arg
 20 25 30
 gat tat aat aga gaa tgt gag att tgc cct tat tgc gat gct aaa aaa 144
 Asp Tyr Asn Arg Glu Cys Glu Ile Cys Pro Tyr Cys Asp Ala Lys Lys
 35 40 45
 cct gtc aga ctt gta gca aca agt tat tac caa aag agc gaa gtt ttt 192
 Pro Val Arg Leu Val Ala Thr Ser Tyr Tyr Gln Lys Ser Glu Val Phe
 50 55 60
 tat ttt gtc tcg aat ttt aca gac cct att ttt tta ccg aca acc tta 240
 Tyr Phe Val Ser Asn Phe Thr Asp Pro Ile Phe Leu Pro Thr Thr Leu
 65 70 75 80
 ttt aag ggg att gaa gtg gtt aaa agc gaa tgg gag ttt gca gag att 288
 Phe Lys Gly Ile Glu Val Val Lys Ser Glu Trp Glu Phe Ala Glu Ile

85 90 95
 gct aat aat ata ttg att ttt cat cat gac ata caa caa gaa aag att 336
 Ala Asn Asn Ile Leu Ile Phe His His Asp Ile Gln Gln Glu Lys Ile
 100 105 110
 ctc att aat aat aaa aga ttg gat cac tat agg ata gaa ata gat tta 384
 Leu Ile Asn Asn Lys Arg Leu Asp His Tyr Arg Ile Glu Ile Asp Leu
 115 120 125
 gaa aaa gaa ttg act att tca tac aat ggt ttt tta att aag gtt caa 432
 Glu Lys Glu Leu Thr Ile Ser Tyr Asn Gly Phe Leu Ile Lys Val Gln
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 aaa tgc 438
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 Asp Tyr Asn Arg Glu Cys Glu Ile Cys Pro Tyr Cys Asp Ala Lys Lys
 35 40 45
 Pro Val Arg Leu Val Ala Thr Ser Tyr Tyr Gln Lys Ser Glu Val Phe
 50 55 60
 Tyr Phe Val Ser Asn Phe Thr Asp Pro Ile Phe Leu Pro Thr Thr Leu
 65 70 75 80
 Phe Lys Gly Ile Glu Val Val Lys Ser Glu Trp Glu Phe Ala Glu Ile
 85 90 95
 Ala Asn Asn Ile Leu Ile Phe His His Asp Ile Gln Gln Glu Lys Ile
 100 105 110
 Leu Ile Asn Asn Lys Arg Leu Asp His Tyr Arg Ile Glu Ile Asp Leu
 115 120 125
 Glu Lys Glu Leu Thr Ile Ser Tyr Asn Gly Phe Leu Ile Lys Val Gln
 130 135 140
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 1 5 10 15
 acg ctt ttt gtg atc ggg ttt atg agc tgc tcg gca agg ctg cct att 96
 Thr Leu Phe Val Ile Gly Phe Met Ser Cys Ser Ala Arg Leu Pro Ile
 20 25 30
 tat gtg ctg ttt gta ggc tcg ttt ttc cct tct tca agt gct ggg ttt 144
 Tyr Val Leu Phe Val Gly Ser Phe Phe Pro Ser Ser Ser Ala Gly Phe
 35 40 45
 gtg ctg ttt tgc att tat att ttg ggg gcg gtt gtg gcg tta gtg atg 192
 Val Leu Phe Cys Ile Tyr Ile Leu Gly Ala Val Val Ala Leu Val Met
 50 55 60
 gcc aaa tta ctc aaa tta agc gtg ttt aaa gga caa acc gaa tct ttt 240
 Ala Lys Leu Leu Lys Leu Ser Val Phe Lys Gly Gln Thr Glu Ser Phe
 65 70 75 80

atc atg gaa atg ccc aaa tac cgc ttt ccc agt tgg aga atg gtc tat 288
 Ile Met Glu Met Pro Lys Tyr Arg Phe Pro Ser Trp Arg Met Val Tyr
 85 90 95
 ttc agt atc tac acc aaa tcg ctt tct tac ctt aaa aag gct ggg act 336
 Phe Ser Ile Tyr Thr Lys Ser Leu Ser Tyr Leu Lys Lys Ala Gly Thr
 100 105 110
 tac att tta gtg gga gcg att tta atc tgg ttt atg tct caa tac cct 384
 Tyr Ile Leu Val Gly Ala Ile Leu Ile Trp Phe Met Ser Gln Tyr Pro
 115 120 125
 aaa agc gat gcg gcc atg aaa gct tat aaa caa gaa agc ttg tta gtg 432
 Lys Ser Asp Ala Ala Met Lys Ala Tyr Lys Gln Glu Ser Leu Leu Val
 130 135 140
 aat aag gat acc act ctt tca agc gaa gct aaa gaa gaa aaa tta aaa 480
 Asn Lys Asp Thr Thr Leu Ser Ser Glu Ala Lys Glu Glu Lys Leu Lys
 145 150 155 160
 gaa tta aaa aca gaa ttg gat aaa aag aat tta aaa aat agc att gta 528
 Glu Leu Lys Thr Glu Leu Asp Lys Lys Asn Leu Lys Asn Ser Ile Val
 165 170 175
 gga aga ggc ggg gcg tat tta gaa aaa gtc ttt agc cct atg gat ttt 576
 Gly Arg Gly Gly Ala Tyr Leu Glu Lys Val Phe Ser Pro Met Asp Phe
 180 185 190
 gat tgg cgt ttg agt gtg tcg ctt gta acc gga ttt atg gct aaa gag 624
 Asp Trp Arg Leu Ser Val Ser Leu Val Thr Gly Phe Met Ala Lys Glu
 195 200 205
 gtg gtg gtt tct act ttg ggc gtg ttg ttt tct tta ggg gat caa aat 672
 Val Val Val Ser Thr Leu Gly Val Leu Phe Ser Leu Gly Asp Gln Asn
 210 215 220
 gaa aaa tct gac gct ttt aga ggg att tta aga aaa gaa gtc agc gtg 720
 Glu Lys Ser Asp Ala Phe Arg Gly Ile Leu Arg Lys Glu Val Ser Val
 225 230 235 240
 cct agc gga atc gct ttt atc gtg ttt gtg atg ttt tat atc cct tgt 768
 Pro Ser Gly Ile Ala Phe Ile Val Phe Val Met Phe Tyr Ile Pro Cys
 245 250 255
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 Phe Ala Ala Thr Ile Thr Phe Gly Arg Glu Ala Gly Gly Ile Lys Phe
 260 265 270
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 Val Ala Tyr Leu Phe Ile Phe Thr Thr Val Val Ala Tyr Ala Phe Ser
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<213> *Helicobacter pylori*

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 35 40 45
 Val Leu Phe Cys Ile Tyr Ile Leu Gly Ala Val Val Ala Leu Val Met
 50 55 60
 Ala Lys Leu Leu Lys Leu Ser Val Phe Lys Gly Gln Thr Glu Ser Phe
 65 70 75 80
 Ile Met Glu Met Pro Lys Tyr Arg Phe Pro Ser Trp Arg Met Val Tyr
 85 90 95
 Phe Ser Ile Tyr Thr Lys Ser Leu Ser Tyr Leu Lys Lys Ala Gly Thr
 100 105 110

Tyr Ile Leu Val Gly Ala Ile Leu Ile Trp Phe Met Ser Gln Tyr Pro
 115 120 125
 Lys Ser Asp Ala Ala Met Lys Ala Tyr Lys Gln Glu Ser Leu Leu Val
 130 135 140
 Asn Lys Asp Thr Thr Leu Ser Ser Glu Ala Lys Glu Glu Lys Leu Lys
 145 150 155 160
 Glu Leu Lys Thr Glu Leu Asp Lys Lys Asn Leu Lys Asn Ser Ile Val
 165 170 175
 Gly Arg Gly Gly Ala Tyr Leu Glu Lys Val Phe Ser Pro Met Asp Phe
 180 185 190
 Asp Trp Arg Leu Ser Val Ser Leu Val Thr Gly Phe Met Ala Lys Glu
 195 200 205
 Val Val Val Ser Thr Leu Gly Val Leu Phe Ser Leu Gly Asp Gln Asn
 210 215 220
 Glu Lys Ser Asp Ala Phe Arg Gly Ile Leu Arg Lys Glu Val Ser Val
 225 230 235 240
 Pro Ser Gly Ile Ala Phe Ile Val Phe Val Met Phe Tyr Ile Pro Cys
 245 250 255
 Phe Ala Ala Thr Ile Thr Phe Gly Arg Glu Ala Gly Gly Ile Lys Phe
 260 265 270
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<213> Helicobacter pylori

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 Glu Ala Cys Ala Lys Asn Phe Gly Ala Phe Cys Val Phe Val Gly Ile
 20 25 30
 gtg aga aaa gag gat aac att caa ggc ttg agt ttt gat att tat gaa 144
 Val Arg Lys Glu Asp Asn Ile Gln Gly Leu Ser Phe Asp Ile Tyr Glu
 35 40 45
 gcg cta tta aag act tgg ttt gaa aaa tgg cac cat aaa gcc aaa gat 192
 Ala Leu Leu Lys Thr Trp Phe Glu Lys Trp His His Lys Ala Lys Asp
 50 55 60
 ttg ggc gtg gtg tta aaa atg gcg cac agc ctg ggc gat gtt ttg ata 240
 Leu Gly Val Val Leu Lys Met Ala His Ser Leu Gly Asp Val Leu Ile
 65 70 75 80
 gga caa agc tca ttt tta tgc gtt tca atg gga aag aat aga aaa aat 288
 Gly Gln Ser Ser Phe Leu Cys Val Ser Met Gly Lys Asn Arg Lys Asn
 85 90 95
 gcc tta gaa cta tac gaa aat ttt att gaa gat ttt aag cat aac gct 336
 Ala Leu Glu Leu Tyr Glu Asn Phe Ile Glu Asp Phe Lys His Asn Ala
 100 105 110
 cct att tgg aaa tac gat tta atc cat aat aaa cgc att tat gct aaa 384
 Pro Ile Trp Lys Tyr Asp Leu Ile His Asn Lys Arg Ile Tyr Ala Lys
 115 120 125
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<213> Helicobacter pylori

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          20           25           30
Val Arg Lys Glu Asp Asn Ile Gln Gly Leu Ser Phe Asp Ile Tyr Glu
          35           40           45
Ala Leu Leu Lys Thr Trp Phe Glu Lys Trp His His Lys Ala Lys Asp
          50           55           60
Leu Gly Val Val Leu Lys Met Ala His Ser Leu Gly Asp Val Leu Ile
          65           70           75           80
Gly Gln Ser Ser Phe Leu Cys Val Ser Met Gly Lys Asn Arg Lys Asn
          85           90           95
Ala Leu Glu Leu Tyr Glu Asn Phe Ile Glu Asp Phe Lys His Asn Ala
          100          105          110
Pro Ile Trp Lys Tyr Asp Leu Ile His Asn Lys Arg Ile Tyr Ala Lys
          115          120          125
Glu Arg Ser His Pro Leu Lys Gly Ser Gly Leu Leu Ala
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<213> Helicobacter pylori

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<222> (1)..(216)

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 1           5           10           15
aaa gcg aat gat ttg aag gaa tta aga gcg att tta caa gaa aaa gag 96
Lys Ala Asn Asp Leu Lys Glu Leu Arg Ala Ile Leu Gln Glu Lys Glu
          20           25           30
ggc tta aaa gag tgg ttg ggc gtt tgc gcg ata gcc ctt aat gat cat 144
Gly Leu Lys Glu Trp Leu Gly Val Cys Ala Ile Ala Leu Asn Asp His
          35           40           45
tta ata gac aat tta aac acg cct tta aaa gat ggc gat gta ata agt 192
Leu Ile Asp Asn Leu Asn Thr Pro Leu Lys Asp Gly Asp Val Ile Ser
          50           55           60
ttg ttg cca ccg gtt tgt ggg ggc 216
Leu Leu Pro Pro Val Cys Gly Gly
          65           70

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<212> PRT

<213> Helicobacter pylori

<400> 16

```

Val Glu Val Arg Phe Phe Gly Pro Ile Lys Glu Glu Asn Phe Phe Ile
 1           5           10           15
Lys Ala Asn Asp Leu Lys Glu Leu Arg Ala Ile Leu Gln Glu Lys Glu
          20           25           30
Gly Leu Lys Glu Trp Leu Gly Val Cys Ala Ile Ala Leu Asn Asp His
          35           40           45
Leu Ile Asp Asn Leu Asn Thr Pro Leu Lys Asp Gly Asp Val Ile Ser
          50           55           60
Leu Leu Pro Pro Val Cys Gly Gly
          65           70

```

<210> 17

<211> 156

<212> DNA

<213> Helicobacter pylori

<220>

<221> CDS

<222> (1)..(156)

<400> 17

```

aac gag caa aaa cag caa ttg att gaa ggg gtt tca gat ttg atg gtt 48
Asn Glu Gln Lys Gln Gln Leu Ile Glu Gly Val Ser Asp Leu Met Val
 1             5             10             15
aag gtg ctg aat aaa aat aag gct tct att gtg gtc att ata gat gag 96
Lys Val Leu Asn Lys Asn Lys Ala Ser Ile Val Val Ile Ile Asp Glu
             20             25             30
gtc gat tct aat aat tat ggt ctt ggg ggc gag agc gtc cat cat ttg 144
Val Asp Ser Asn Asn Tyr Gly Leu Gly Gly Glu Ser Val His His Leu
             35             40             45
agg caa aaa aac 156
Arg Gln Lys Asn
 50

```

<210> 18

<211> 52

<212> PRT

<213> Helicobacter pylori

<400> 18

```

Asn Glu Gln Lys Gln Gln Leu Ile Glu Gly Val Ser Asp Leu Met Val
 1             5             10             15
Lys Val Leu Asn Lys Asn Lys Ala Ser Ile Val Val Ile Ile Asp Glu
             20             25             30
Val Asp Ser Asn Asn Tyr Gly Leu Gly Gly Glu Ser Val His His Leu
             35             40             45
Arg Gln Lys Asn
 50

```

<210> 19

<211> 600

<212> DNA

<213> Helicobacter pylori

<220>

<221> CDS

<222> (1)..(600)

<400> 19

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att tat gcg cct att tta gcc ggg ctt gcc tct aat aac aaa tac tct 48
Ile Tyr Ala Pro Ile Leu Ala Gly Leu Ala Ser Asn Asn Lys Tyr Ser
 1             5             10             15
tta att ggc tcc gca aga gcg acg atc caa ctg ctc agc ttt gaa gtg 96
Leu Ile Gly Ser Ala Arg Ala Thr Ile Gln Leu Leu Ser Phe Glu Val
             20             25             30
gtc agc act tta acc att cta gcc ccc tta atg gtg gta gga tgc ctc 144
Val Ser Thr Leu Thr Ile Leu Ala Pro Leu Met Val Val Gly Ser Leu
             35             40             45
tct tta gtg gaa atc aat cat tac caa agc ggt ggg ttt tta gac tgg 192
Ser Leu Val Glu Ile Asn His Tyr Gln Ser Gly Gly Phe Leu Asp Trp
             50             55             60
ctt gtg ttt aag cag cct cta gcg ttt gtt ttg ttt ttg atc gca agt 240
Leu Val Phe Lys Gln Pro Leu Ala Phe Val Leu Phe Leu Ile Ala Ser
             65             70             75             80
tat gcc gaa ttg aat cga acc ccc ttt gac ttg cta gag cat gaa gcc 288
Tyr Ala Glu Leu Asn Arg Thr Pro Phe Asp Leu Leu Glu His Glu Ala
             85             90             95
gag atc gtg gcg ggg tat tgc acc gaa tac agc ggc ttg aaa tgg ggc 336
Glu Ile Val Ala Gly Tyr Cys Thr Glu Tyr Ser Gly Leu Lys Trp Gly
             100             105             110
atg ttc ttt tta gcg gaa tac gcg cat tta ttc gct ttt tct ttt gtg 384

```

Met Phe Phe Leu Ala Glu Tyr Ala His Leu Phe Ala Phe Ser Phe Val
 115 120 125
 att tct att gtg ttt ttt ggc ggg ttt aac gca tgg ggc ttt atc cct 432
 Ile Ser Ile Val Phe Phe Gly Gly Phe Asn Ala Trp Gly Phe Ile Pro
 130 135 140
 gga ggc ata gcg att ttg att aaa gcg ggc ttt ttt gtc ttt tta tcc 480
 Gly Gly Ile Ala Ile Leu Ile Lys Ala Gly Phe Phe Val Phe Leu Ser
 145 150 155 160
 atg tgg gtt aga gcg act tat ccg cat gtg cgc cca gac caa ctg atg 528
 Met Trp Val Arg Ala Thr Tyr Pro His Val Arg Pro Asp Gln Leu Met
 165 170 175
 gat atg tgc tgg aaa atc atg ctg cct tta gcg tta ttg aac att gtg 576
 Asp Met Cys Trp Lys Ile Met Leu Pro Leu Ala Leu Leu Asn Ile Val
 180 185 190
 cta acg ggc att atc att tta att 600
 Leu Thr Gly Ile Ile Ile Leu Ile
 195 200

<210> 20

<211> 200

<212> PRT

<213> Helicobacter pylori

<400> 20

Ile Tyr Ala Pro Ile Leu Ala Gly Leu Ala Ser Asn Asn Lys Tyr Ser
 1 5 10 15
 Leu Ile Gly Ser Ala Arg Ala Thr Ile Gln Leu Leu Ser Phe Glu Val
 20 25 30
 Val Ser Thr Leu Thr Ile Leu Ala Pro Leu Met Val Val Gly Ser Leu
 35 40 45
 Ser Leu Val Glu Ile Asn His Tyr Gln Ser Gly Gly Phe Leu Asp Trp
 50 55 60
 Leu Val Phe Lys Gln Pro Leu Ala Phe Val Leu Phe Leu Ile Ala Ser
 65 70 75 80
 Tyr Ala Glu Leu Asn Arg Thr Pro Phe Asp Leu Leu Glu His Glu Ala
 85 90 95
 Glu Ile Val Ala Gly Tyr Cys Thr Glu Tyr Ser Gly Leu Lys Trp Gly
 100 105 110
 Met Phe Phe Leu Ala Glu Tyr Ala His Leu Phe Ala Phe Ser Phe Val
 115 120 125
 Ile Ser Ile Val Phe Phe Gly Gly Phe Asn Ala Trp Gly Phe Ile Pro
 130 135 140
 Gly Gly Ile Ala Ile Leu Ile Lys Ala Gly Phe Phe Val Phe Leu Ser
 145 150 155 160
 Met Trp Val Arg Ala Thr Tyr Pro His Val Arg Pro Asp Gln Leu Met
 165 170 175
 Asp Met Cys Trp Lys Ile Met Leu Pro Leu Ala Leu Leu Asn Ile Val
 180 185 190
 Leu Thr Gly Ile Ile Ile Leu Ile
 195 200

<210> 21

<211> 474

<212> DNA

<213> Helicobacter pylori

<220>

<221> CDS

<222> (1)..(474)

<400> 21

gac gcc aag gct caa gaa gtg gcg atg tgc gta gcg atg ggt aaa acc 48
 Asp Ala Lys Ala Gln Glu Val Ala Met Cys Val Ala Met Gly Lys Thr
 1 5 10 15
 cta aac gat aag ggg cgc ttg aaa cac tcc gtg cat gag ttt tac att 96
 Leu Asn Asp Lys Gly Arg Leu Lys His Ser Val His Glu Phe Tyr Ile


```

      20      25      30
aaa tcc ccc gaa gaa atg gca aag ctc ttt gca gat att cca gaa gct 144
Lys Ser Pro Glu Glu Met Ala Lys Leu Phe Ala Asp Ile Pro Glu Ala
      35      40      45
tta gaa aac acc caa gaa atc gct gat aaa tgc gtt tta gag att gat 192
Leu Glu Asn Thr Gln Glu Ile Ala Asp Lys Cys Val Leu Glu Ile Asp
      50      55      60
tta aaa gac gat aaa aag aac ccc cca acc ccc cca agc ttc aaa ttc 240
Leu Lys Asp Asp Lys Lys Asn Pro Pro Thr Pro Pro Ser Phe Lys Phe
      65      70      75      80
act aaa gct tac gct caa aat gag ggg ctg aat ttt gaa gat gac gct 288
Thr Lys Ala Tyr Ala Gln Asn Glu Gly Leu Asn Phe Glu Asp Asp Ala
      85      90      95
tct tat ttt gcc tat aag gct aga gaa ggc ttg aaa gag cgc tta gtt 336
Ser Tyr Phe Ala Tyr Lys Ala Arg Glu Gly Leu Lys Glu Arg Leu Val
      100      105      110
tta gta cca aaa gaa aag cat gat caa tat aaa gag cgc cta gaa aaa 384
Leu Val Pro Lys Glu Lys His Asp Gln Tyr Lys Glu Arg Leu Glu Lys
      115      120      125
gaa att gaa gtc att acg aac atg aaa ttc cca ggg tat atg ctg att 432
Glu Ile Glu Val Ile Thr Asn Met Lys Phe Pro Gly Tyr Met Leu Ile
      130      135      140
gtg tgg gat ttt atc cgt tat gct aag gaa atg ggc att cct 474
Val Trp Asp Phe Ile Arg Tyr Ala Lys Glu Met Gly Ile Pro
      145      150      155

```

<210> 22

<211> 158

<212> PRT

<213> *Helicobacter pylori*

<400> 22

```

Asp Ala Lys Ala Gln Glu Val Ala Met Cys Val Ala Met Gly Lys Thr
1      5      10      15
Leu Asn Asp Lys Gly Arg Leu Lys His Ser Val His Glu Phe Tyr Ile
      20      25      30
Lys Ser Pro Glu Glu Met Ala Lys Leu Phe Ala Asp Ile Pro Glu Ala
      35      40      45
Leu Glu Asn Thr Gln Glu Ile Ala Asp Lys Cys Val Leu Glu Ile Asp
      50      55      60
Leu Lys Asp Asp Lys Lys Asn Pro Pro Thr Pro Pro Ser Phe Lys Phe
      65      70      75      80
Thr Lys Ala Tyr Ala Gln Asn Glu Gly Leu Asn Phe Glu Asp Asp Ala
      85      90      95
Ser Tyr Phe Ala Tyr Lys Ala Arg Glu Gly Leu Lys Glu Arg Leu Val
      100      105      110
Leu Val Pro Lys Glu Lys His Asp Gln Tyr Lys Glu Arg Leu Glu Lys
      115      120      125
Glu Ile Glu Val Ile Thr Asn Met Lys Phe Pro Gly Tyr Met Leu Ile
      130      135      140
Val Trp Asp Phe Ile Arg Tyr Ala Lys Glu Met Gly Ile Pro
      145      150      155

```

<210> 23

<211> 512

<212> DNA

<213> *Helicobacter pylori*

<220>

<221> CDS

<222> (1)..(510)

<400> 23

```

aag aat aaa gca ttc cac aac att gcc ctt gat att gaa acc cta aac 48
Lys Asn Lys Ala Phe His Asn Ile Ala Leu Asp Ile Glu Thr Leu Asn
1      5      10      15

```

```

caa gaa gcc cta aaa aac act tat gat gtg agc gca atc agc ttt ggg 96
Gln Glu Ala Leu Lys Asn Thr Tyr Asp Val Ser Ala Ile Ser Phe Gly
      20      25      30
tta tac cct aaa att gcg aac gat tac gcc tta ctc ccc acg gca acg 144
Leu Tyr Pro Lys Ile Ala Asn Asp Tyr Ala Leu Leu Pro Thr Ala Thr
      35      40      45
agc ttt ggg aat ggc tat ggg cct aaa tta gtg aaa aaa aag ggc gtg 192
Ser Phe Gly Asn Gly Tyr Gly Pro Lys Leu Val Lys Lys Lys Gly Val
      50      55      60
aaa ttg aaa aaa gat ttt aga gtc gca tta agt ggg gag cac acc acc 240
Lys Leu Lys Lys Asp Phe Arg Val Ala Leu Ser Gly Glu His Thr Thr
      65      70      75      80
aac gcc ctc ttg ttt aag atc tat tac aaa cat gcg cgc atc act tat 288
Asn Ala Leu Leu Phe Lys Ile Tyr Tyr Lys His Ala Arg Ile Thr Tyr
      85      90      95
atg aat ttt tta gac att gaa aaa gcg gtt ttg gaa gaa aaa gtg cat 336
Met Asn Phe Leu Asp Ile Glu Lys Ala Val Leu Glu Glu Lys Val His
      100      105      110
gcg ggc gta ttg atc cat gag agt atc ttg gat ttt cat aat gaa tta 384
Ala Gly Val Leu Ile His Glu Ser Ile Leu Asp Phe His Asn Glu Leu
      115      120      125
gaa gtg gaa aaa gaa ttg tgg gat gtt tgg aaa gaa ctc att gaa gtg 432
Glu Val Glu Lys Glu Leu Trp Asp Val Trp Lys Glu Leu Ile Glu Val
      130      135      140
gat ttg ccc ttg cct tta ggg ggc atg gcg atc agg cga tct atc ccc 480
Asp Leu Pro Leu Pro Leu Gly Gly Met Ala Ile Arg Arg Ser Ile Pro
      145      150      155      160
ttg tat cgc gcg att ttg att aaa aag gct tt 512
Leu Tyr Arg Ala Ile Leu Ile Lys Lys Ala
      165      170

```

<210> 24

<211> 170

<212> PRT

<213> Helicobacter pylori

<400> 24

```

Lys Asn Lys Ala Phe His Asn Ile Ala Leu Asp Ile Glu Thr Leu Asn
  1      5      10      15
Gln Glu Ala Leu Lys Asn Thr Tyr Asp Val Ser Ala Ile Ser Phe Gly
      20      25      30
Leu Tyr Pro Lys Ile Ala Asn Asp Tyr Ala Leu Leu Pro Thr Ala Thr
      35      40      45
Ser Phe Gly Asn Gly Tyr Gly Pro Lys Leu Val Lys Lys Lys Gly Val
      50      55      60
Lys Leu Lys Lys Asp Phe Arg Val Ala Leu Ser Gly Glu His Thr Thr
      65      70      75      80
Asn Ala Leu Leu Phe Lys Ile Tyr Tyr Lys His Ala Arg Ile Thr Tyr
      85      90      95
Met Asn Phe Leu Asp Ile Glu Lys Ala Val Leu Glu Glu Lys Val His
      100      105      110
Ala Gly Val Leu Ile His Glu Ser Ile Leu Asp Phe His Asn Glu Leu
      115      120      125
Glu Val Glu Lys Glu Leu Trp Asp Val Trp Lys Glu Leu Ile Glu Val
      130      135      140
Asp Leu Pro Leu Pro Leu Gly Gly Met Ala Ile Arg Arg Ser Ile Pro
      145      150      155      160
Leu Tyr Arg Ala Ile Leu Ile Lys Lys Ala
      165      170

```

<210> 25

<211> 432

<212> DNA

<213> Helicobacter pylori

<220>

<221> CDS

<222> (1)..(432)

<400> 25

```

tta aaa atc att caa ggg gca tta gat act agg gag ctt tta aaa gcc 48
Leu Lys Ile Ile Gln Gly Ala Leu Asp Thr Arg Glu Leu Leu Lys Ala
  1           5           10           15
tac caa gag gaa gct tgc gcg aaa aac ttt gga gcg ttt tgt gtg ttt 96
Tyr Gln Glu Glu Ala Cys Ala Lys Asn Phe Gly Ala Phe Cys Val Phe
          20           25           30
gtg ggg att gtg aga aaa gag gat aac att caa ggc ttg agt ttt gat 144
Val Gly Ile Val Arg Lys Glu Asp Asn Ile Gln Gly Leu Ser Phe Asp
          35           40           45
att tat gaa gcg cta tta aag act tgg ttt gaa aaa tgg cac cat aaa 192
Ile Tyr Glu Ala Leu Leu Lys Thr Trp Phe Glu Lys Trp His His Lys
          50           55           60
gcc aaa gat ttg ggc gtg gtg tta aaa atg gcg cac agc ctg gcc gat 240
Ala Lys Asp Leu Gly Val Val Leu Lys Met Ala His Ser Leu Gly Asp
          65           70           75           80
gtt ttg ata gga caa agc tca ttt tta tgc gtt tca atg gga aag aat 288
Val Leu Ile Gly Gln Ser Ser Phe Leu Cys Val Ser Met Gly Lys Asn
          85           90           95
aga aaa aat gcc tta gaa cta tac gaa aat ttt att gaa gat ttt aag 336
Arg Lys Asn Ala Leu Glu Leu Tyr Glu Asn Phe Ile Glu Asp Phe Lys
          100           105           110
cat aac gct cct att tgg aaa tac gat tta atc cat aat aaa cgc att 384
His Asn Ala Pro Ile Trp Lys Tyr Asp Leu Ile His Asn Lys Arg Ile
          115           120           125
tat gct aaa gaa aga agc cac cct tta aaa ggg agc ggg ctt tta gct 432
Tyr Ala Lys Glu Arg Ser His Pro Leu Lys Gly Ser Gly Leu Leu Ala
          130           135           140

```

<210> 26

<211> 144

<212> PRT

<213> *Helicobacter pylori*

<400> 26

```

Leu Lys Ile Ile Gln Gly Ala Leu Asp Thr Arg Glu Leu Leu Lys Ala
  1           5           10           15
Tyr Gln Glu Glu Ala Cys Ala Lys Asn Phe Gly Ala Phe Cys Val Phe
          20           25           30
Val Gly Ile Val Arg Lys Glu Asp Asn Ile Gln Gly Leu Ser Phe Asp
          35           40           45
Ile Tyr Glu Ala Leu Leu Lys Thr Trp Phe Glu Lys Trp His His Lys
          50           55           60
Ala Lys Asp Leu Gly Val Val Leu Lys Met Ala His Ser Leu Gly Asp
          65           70           75           80
Val Leu Ile Gly Gln Ser Ser Phe Leu Cys Val Ser Met Gly Lys Asn
          85           90           95
Arg Lys Asn Ala Leu Glu Leu Tyr Glu Asn Phe Ile Glu Asp Phe Lys
          100           105           110
His Asn Ala Pro Ile Trp Lys Tyr Asp Leu Ile His Asn Lys Arg Ile
          115           120           125
Tyr Ala Lys Glu Arg Ser His Pro Leu Lys Gly Ser Gly Leu Leu Ala
          130           135           140

```

<210> 27

<211> 516

<212> DNA

<213> *Helicobacter pylori*

<220>

<221> CDS

<222> (1)..(516)

<400> 27

```

tta agc ttt agc gcg gat aaa ttc ttt aac agt gcg caa gcg ggc att 48
Leu Ser Phe Ser Ala Asp Lys Phe Phe Asn Ser Ala Gln Ala Gly Ile
1 5 10 15
att atg ggg caa aaa gaa cgg gtt gaa gcg tta aaa aac cac ccc ctt 96
Ile Met Gly Gln Lys Glu Arg Val Glu Ala Leu Lys Asn His Pro Leu
20 25 30
tat aga gtt tta agg gtg ggt aaa atc acg ctc acc ttg ctt ttt tgc 144
Tyr Arg Val Leu Arg Val Gly Lys Ile Thr Leu Thr Leu Leu Phe Cys
35 40 45
agc cta aaa gca tgg ata aat cat caa gaa gac att aca atc cat gcg 192
Ser Leu Lys Ala Trp Ile Asn His Gln Glu Asp Ile Thr Ile His Ala
50 55 60
tta ttg aac caa act aaa gac gca tta ttg caa aaa gcc ctc aaa ctc 240
Leu Leu Asn Gln Thr Lys Asp Ala Leu Leu Gln Lys Ala Leu Lys Leu
65 70 75 80
tac gct ctt tta aag cct tta gaa ttg aat gtg agc ata gcc tct agc 288
Tyr Ala Leu Leu Lys Pro Leu Glu Leu Asn Val Ser Ile Ala Ser Ser
85 90 95
ttt tct aaa ata ggg aat ttg ttt ggt agg gaa tta gaa tcc ttt tgc 336
Phe Ser Lys Ile Gly Asn Leu Phe Gly Arg Glu Leu Glu Ser Phe Cys
100 105 110
gtg aaa atc cag ccc aaa aac acc cgt gct tta aat agt gag aaa ctt 384
Val Lys Ile Gln Pro Lys Asn Thr Arg Ala Leu Asn Ser Glu Lys Leu
115 120 125
tat tta aag ctt ttc caa aaa ggc gtt atc gca agg att tca tgc gaa 432
Tyr Leu Lys Leu Phe Gln Lys Gly Val Ile Ala Arg Ile Ser Cys Glu
130 135 140
ttc gtg tgc ttt gaa gtc ttt agc ttg aat gaa aaa gat ttt gaa aaa 480
Phe Val Cys Phe Glu Val Phe Ser Leu Asn Glu Lys Asp Phe Glu Lys
145 150 155 160
atc gct ctg gtt tta gaa gaa att ctt aat aaa gct 516
Ile Ala Leu Val Leu Glu Glu Ile Leu Asn Lys Ala
165 170

```

<210> 28

<211> 172

<212> PRT

<213> *Helicobacter pylori*

<400> 28

```

Leu Ser Phe Ser Ala Asp Lys Phe Phe Asn Ser Ala Gln Ala Gly Ile
1 5 10 15
Ile Met Gly Gln Lys Glu Arg Val Glu Ala Leu Lys Asn His Pro Leu
20 25 30
Tyr Arg Val Leu Arg Val Gly Lys Ile Thr Leu Thr Leu Leu Phe Cys
35 40 45
Ser Leu Lys Ala Trp Ile Asn His Gln Glu Asp Ile Thr Ile His Ala
50 55 60
Leu Leu Asn Gln Thr Lys Asp Ala Leu Leu Gln Lys Ala Leu Lys Leu
65 70 75 80
Tyr Ala Leu Leu Lys Pro Leu Glu Leu Asn Val Ser Ile Ala Ser Ser
85 90 95
Phe Ser Lys Ile Gly Asn Leu Phe Gly Arg Glu Leu Glu Ser Phe Cys
100 105 110
Val Lys Ile Gln Pro Lys Asn Thr Arg Ala Leu Asn Ser Glu Lys Leu
115 120 125
Tyr Leu Lys Leu Phe Gln Lys Gly Val Ile Ala Arg Ile Ser Cys Glu
130 135 140
Phe Val Cys Phe Glu Val Phe Ser Leu Asn Glu Lys Asp Phe Glu Lys
145 150 155 160
Ile Ala Leu Val Leu Glu Glu Ile Leu Asn Lys Ala
165 170

```

<210> 29

<211> 444

<212> DNA

<213> *Helicobacter pylori*

<220>

<221> CDS

<222> (1)..(444)

<400> 29

```

atc att act caa gct aga aag gct aat ggg gtg att gtt cta gcc tta 48
Ile Ile Thr Gln Ala Arg Lys Ala Asn Gly Val Ile Val Leu Ala Leu
1 5 10 15
caa gac att aac caa cta agc gaa gtg aga aac gct caa agc ttt ata 96
Gln Asp Ile Asn Gln Leu Ser Glu Val Arg Asn Ala Gln Ser Phe Ile
20 25 30
aaa aat atg ggg caa ttg att ttg tat ccc caa aga aat att gat acc 144
Lys Asn Met Gly Gln Leu Ile Leu Tyr Pro Gln Arg Asn Ile Asp Thr
35 40 45
aaa gat tta aac gat aaa ttt ggc att aga cta agc gat aca gaa aaa 192
Lys Asp Leu Asn Asp Lys Phe Gly Ile Arg Leu Ser Asp Thr Glu Lys
50 55 60
cat ttt tta gaa aac acc gcc gtt aat gaa tac aaa gtc tta ctc aaa 240
His Phe Leu Glu Asn Thr Ala Val Asn Glu Tyr Lys Val Leu Leu Lys
65 70 75 80
aac atg aat gat ggc tca tct aac att ata gat gtg agc cta agt tct 288
Asn Met Asn Asp Gly Ser Ser Asn Ile Ile Asp Val Ser Leu Ser Ser
85 90 95
ttg ggt aat tac cta caa atc ttt agc tct aat tct agc atg gta gaa 336
Leu Gly Asn Tyr Leu Gln Ile Phe Ser Ser Asn Ser Ser Met Val Glu
100 105 110
cac att gat aat ctc att aag cat tac cct aaa act tgg cga gaa gtc 384
His Ile Asp Asn Leu Ile Lys His Tyr Pro Lys Thr Trp Arg Glu Val
115 120 125
ttt gtg agt aac aaa cac gaa aat ttt gat gac aaa aaa cac tta gaa 432
Phe Val Ser Asn Lys His Glu Asn Phe Asp Asp Lys Lys His Leu Glu
130 135 140
aag gtg ctt aaa 444
Lys Val Leu Lys
145

```

<210> 30

<211> 148

<212> PRT

<213> *Helicobacter pylori*

<400> 30

```

Ile Ile Thr Gln Ala Arg Lys Ala Asn Gly Val Ile Val Leu Ala Leu
1 5 10 15
Gln Asp Ile Asn Gln Leu Ser Glu Val Arg Asn Ala Gln Ser Phe Ile
20 25 30
Lys Asn Met Gly Gln Leu Ile Leu Tyr Pro Gln Arg Asn Ile Asp Thr
35 40 45
Lys Asp Leu Asn Asp Lys Phe Gly Ile Arg Leu Ser Asp Thr Glu Lys
50 55 60
His Phe Leu Glu Asn Thr Ala Val Asn Glu Tyr Lys Val Leu Leu Lys
65 70 75 80
Asn Met Asn Asp Gly Ser Ser Asn Ile Ile Asp Val Ser Leu Ser Ser
85 90 95
Leu Gly Asn Tyr Leu Gln Ile Phe Ser Ser Asn Ser Ser Met Val Glu
100 105 110
His Ile Asp Asn Leu Ile Lys His Tyr Pro Lys Thr Trp Arg Glu Val
115 120 125
Phe Val Ser Asn Lys His Glu Asn Phe Asp Asp Lys Lys His Leu Glu
130 135 140

```

Lys Val Leu Lys

145

<210> 31

<211> 426

<212> DNA

<213> Helicobacter pylori

<220>

<221> CDS

<222> (1)..(426)

<400> 31

```

acg gtg ggc gat gtt ttt ggt gaa aac ggg ctt tta aac gcg cta gat 48
Thr Val Gly Asp Val Phe Gly Glu Asn Gly Leu Leu Asn Ala Leu Asp
1 5 10 15
cct acg gaa aga aaa aaa att gat caa atg ctt tta gag caa atc caa 96
Pro Thr Glu Arg Lys Lys Ile Asp Gln Met Leu Leu Glu Gln Ile Gln
20 25 30
gcc cat tct tca ggg ttt gaa aaa ttc atc gtg aaa act tta ggg att 144
Ala His Ser Ser Gly Phe Glu Lys Phe Ile Val Lys Thr Leu Gly Ile
35 40 45
gaa aat gta gag aat ttc atc aat aac tgg tat ggc aag caa agc ttg 192
Glu Asn Val Glu Asn Phe Ile Asn Asn Trp Tyr Gly Lys Gln Ser Leu
50 55 60
agt tct ttt gcc aat aat ttt gtg cct gga ggc ttg aat caa gcc ctt 240
Ser Ser Phe Ala Asn Asn Phe Val Pro Gly Gly Leu Asn Gln Ala Leu
65 70 75 80
gat aaa ata ggc tct agc tct gat gcc aaa gac tta cag aac ttc ttg 288
Asp Lys Ile Gly Ser Ser Ser Asp Ala Lys Asp Leu Gln Asn Phe Leu
85 90 95
gat aaa acg act ttt ggg gat att tta aat caa atg att gaa caa gcc 336
Asp Lys Thr Thr Phe Gly Asp Ile Leu Asn Gln Met Ile Glu Gln Ala
100 105 110
ccc tta atc aat aaa ctc att tct tgg ctg ggt ccg cag gat ttg agc 384
Pro Leu Ile Asn Lys Leu Ile Ser Trp Leu Gly Pro Gln Asp Leu Ser
115 120 125
gtt tta gtg aat atc gct tta aat agc atc act aac cct agt 426
Val Leu Val Asn Ile Ala Leu Asn Ser Ile Thr Asn Pro Ser
130 135 140

```

<210> 32

<211> 142

<212> PRT

<213> Helicobacter pylori

<400> 32

```

Thr Val Gly Asp Val Phe Gly Glu Asn Gly Leu Leu Asn Ala Leu Asp
1 5 10 15
Pro Thr Glu Arg Lys Lys Ile Asp Gln Met Leu Leu Glu Gln Ile Gln
20 25 30
Ala His Ser Ser Gly Phe Glu Lys Phe Ile Val Lys Thr Leu Gly Ile
35 40 45
Glu Asn Val Glu Asn Phe Ile Asn Asn Trp Tyr Gly Lys Gln Ser Leu
50 55 60
Ser Ser Phe Ala Asn Asn Phe Val Pro Gly Gly Leu Asn Gln Ala Leu
65 70 75 80
Asp Lys Ile Gly Ser Ser Ser Asp Ala Lys Asp Leu Gln Asn Phe Leu
85 90 95
Asp Lys Thr Thr Phe Gly Asp Ile Leu Asn Gln Met Ile Glu Gln Ala
100 105 110
Pro Leu Ile Asn Lys Leu Ile Ser Trp Leu Gly Pro Gln Asp Leu Ser
115 120 125
Val Leu Val Asn Ile Ala Leu Asn Ser Ile Thr Asn Pro Ser
130 135 140

```

<210> 33

<211> 357

<212> DNA

<213> Helicobacter pylori

<220>

<221> CDS

<222> (1)..(357)

<400> 33

```

caa gcg cac cat ctt aaa aac ctt ttg gaa gcc ttt tat cac caa aat 48
Gln Ala His His Leu Lys Asn Leu Leu Glu Ala Phe Tyr His Gln Asn
 1           5           10           15
aaa gag agt ttg ggc ttt ttt tcc cct tat ttt agt ttg cga tct caa 96
Lys Glu Ser Leu Gly Phe Phe Ser Pro Tyr Phe Ser Leu Arg Ser Gln
          20           25           30
acc cct agc gtc tct tat gaa agc gcg tta gct tct tta gaa aac tat 144
Thr Pro Ser Val Ser Tyr Glu Ser Ala Leu Ala Ser Leu Glu Asn Tyr
          35           40           45
ttt atg gct ttg ttc caa tcc cat ttt aaa gac gat acc gca ctc caa 192
Phe Met Ala Leu Phe Gln Ser His Phe Lys Asp Asp Thr Ala Leu Gln
          50           55           60
cag aat ttt aaa gga ttg ttg caa gcc ttt gtt tct atg gct aaa gac 240
Gln Asn Phe Lys Gly Leu Leu Gln Ala Phe Val Ser Met Ala Lys Asp
          65           70           75           80
aaa cga tcc caa atc gct ctt aac gcc caa gct aaa gac aac gcc aag 288
Lys Arg Ser Gln Ile Ala Leu Asn Ala Gln Ala Lys Asp Asn Ala Lys
          85           90           95
cta act ttt aac gcc ttg tta gaa agc ctt agc gtg aat ttc ttt caa 336
Leu Thr Phe Asn Ala Leu Leu Glu Ser Leu Ser Val Asn Phe Phe Gln
          100           105           110
tct tac aaa ata agc cat gag 357
Ser Tyr Lys Ile Ser His Glu
          115

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<210> 34

<211> 119

<212> PRT

<213> Helicobacter pylori

<400> 34

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Gln Ala His His Leu Lys Asn Leu Leu Glu Ala Phe Tyr His Gln Asn
 1           5           10           15
Lys Glu Ser Leu Gly Phe Phe Ser Pro Tyr Phe Ser Leu Arg Ser Gln
          20           25           30
Thr Pro Ser Val Ser Tyr Glu Ser Ala Leu Ala Ser Leu Glu Asn Tyr
          35           40           45
Phe Met Ala Leu Phe Gln Ser His Phe Lys Asp Asp Thr Ala Leu Gln
          50           55           60
Gln Asn Phe Lys Gly Leu Leu Gln Ala Phe Val Ser Met Ala Lys Asp
          65           70           75           80
Lys Arg Ser Gln Ile Ala Leu Asn Ala Gln Ala Lys Asp Asn Ala Lys
          85           90           95
Leu Thr Phe Asn Ala Leu Leu Glu Ser Leu Ser Val Asn Phe Phe Gln
          100           105           110
Ser Tyr Lys Ile Ser His Glu
          115

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<210> 35

<211> 980

<212> DNA

<213> Helicobacter pylori

<220>

<221> CDS

<222> (1)..(978)

<400> 35

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gtg ggt tct gga gcc ggg agg aaa gcc agc tct acg gtt tta act ttg 48

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325

<210> 36

<211> 326

<212> PRT

<213> Helicobacter pylori

<400> 36

Val Gly Ser Gly Ala Gly Arg Lys Ala Ser Ser Thr Val Leu Thr Leu
 1 5 10 15
 Gln Ala Ser Glu Gly Ile Thr Ser Ser Lys Asn Ala Glu Ile Ser Leu
 20 25 30
 Tyr Asp Gly Ala Thr Leu Asn Leu Ala Ser Asn Ser Val Lys Leu Met
 35 40 45
 Gly Asn Val Trp Met Gly Arg Leu Gln Tyr Val Gly Ala Tyr Leu Ala
 50 55 60
 Pro Ser Tyr Ser Thr Ile Asn Thr Ser Lys Val Thr Gly Glu Val Asn
 65 70 75 80
 Phe Asn His Leu Thr Val Gly Asp His Asn Ala Ala Gln Ala Gly Ile
 85 90 95
 Ile Ala Ser Asn Lys Thr His Ile Gly Thr Leu Asp Leu Trp Gln Ser
 100 105 110
 Ala Gly Leu Asn Ile Ile Ala Pro Pro Glu Gly Gly Tyr Lys Asp Lys
 115 120 125
 Pro Lys Asp Lys Pro Ser Asn Thr Thr Gln Asn Asn Ala Asn Asn Asn
 130 135 140
 Gln Gln Asn Ser Ala Gln Asn Asn Ser Asn Thr Gln Val Ile Asn Pro
 145 150 155 160
 Pro Asn Ser Ala Gln Lys Thr Glu Ile Gln Pro Thr Gln Val Ile Asp
 165 170 175
 Gly Pro Phe Ala Gly Gly Lys Asp Thr Val Val Asn Ile Asp Arg Ile
 180 185 190
 Asn Thr Asn Ala Asp Gly Thr Ile Lys Val Gly Gly Tyr Lys Ala Ser
 195 200 205
 Leu Thr Thr Asn Ala Ala His Leu His Ile Gly Lys Gly Gly Ile Asn
 210 215 220
 Leu Ser Asn Gln Ala Ser Gly Arg Thr Leu Leu Val Glu Asn Leu Thr
 225 230 235 240
 Gly Asn Ile Thr Val Asp Gly Pro Leu Arg Val Asn Asn Gln Val Gly
 245 250 255
 Gly Tyr Ala Leu Ala Gly Ser Ser Ala Asn Phe Glu Phe Lys Ala Gly
 260 265 270
 Thr Asp Thr Lys Asn Gly Thr Ala Thr Phe Asn Asn Asp Ile Ser Leu
 275 280 285
 Gly Arg Phe Val Asn Leu Lys Val Asp Ala His Thr Ala Asn Phe Lys
 290 295 300
 Gly Ile Asp Thr Gly Asn Gly Gly Phe Asn Thr Leu Asp Phe Ser Gly
 305 310 315 320
 Val Thr Gly Lys Val Asn
 325

<210> 37

<211> 362

<212> DNA

<213> Helicobacter pylori

<220>

<221> CDS

<222> (1)..(360)

<400> 37

agt aat tta tgt ggt aat ggt agt agc ggt agt agt ggc act act tgc 48
 Ser Asn Leu Cys Gly Asn Gly Ser Ser Gly Ser Ser Gly Thr Thr Cys
 1 5 10 15
 tcc ggt tgg ctt atc aac ctt tta ggg gca atc ccc acc aat gga gtg 96
 Ser Gly Trp Leu Ile Asn Leu Leu Gly Ala Ile Pro Thr Asn Gly Val

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      20      25      30
agc gat acg aat aat tta att aat ctg ctc act gaa ttc att aaa acc 144
Ser Asp Thr Asn Asn Leu Ile Asn Leu Leu Thr Glu Phe Ile Lys Thr
      35      40      45
gcc ggg ttt atc caa aat aat gat agt agt gta tct act agt ctt aca 192
Ala Gly Phe Ile Gln Asn Asn Asp Ser Ser Val Ser Thr Ser Leu Thr
      50      55      60
agc gct ttt caa gcc att acg agc gct att tct caa ggg ttt caa gcc 240
Ser Ala Phe Gln Ala Ile Thr Ser Ala Ile Ser Gln Gly Phe Gln Ala
      65      70      75      80
tta caa aac gat att agc cct aat gcg att tta acc ttg ctc caa gag 288
Leu Gln Asn Asp Ile Ser Pro Asn Ala Ile Leu Thr Leu Leu Gln Glu
      85      90      95
att act tct aac acc acc acc att cag tca ttc tcg caa acc tta cgg 336
Ile Thr Ser Asn Thr Thr Thr Ile Gln Ser Phe Ser Gln Thr Leu Arg
      100      105      110
cag ctt tta ggg gat aaa aca ttc tt 362
Gln Leu Leu Gly Asp Lys Thr Phe
      115      120
<210> 38
<211> 120
<212> PRT
<213> Helicobacter pylori
<400> 38
Ser Asn Leu Cys Gly Asn Gly Ser Ser Gly Ser Ser Gly Thr Thr Cys
  1      5      10      15
Ser Gly Trp Leu Ile Asn Leu Leu Gly Ala Ile Pro Thr Asn Gly Val
      20      25      30
Ser Asp Thr Asn Asn Leu Ile Asn Leu Leu Thr Glu Phe Ile Lys Thr
      35      40      45
Ala Gly Phe Ile Gln Asn Asn Asp Ser Ser Val Ser Thr Ser Leu Thr
      50      55      60
Ser Ala Phe Gln Ala Ile Thr Ser Ala Ile Ser Gln Gly Phe Gln Ala
      65      70      75      80
Leu Gln Asn Asp Ile Ser Pro Asn Ala Ile Leu Thr Leu Leu Gln Glu
      85      90      95
Ile Thr Ser Asn Thr Thr Thr Ile Gln Ser Phe Ser Gln Thr Leu Arg
      100      105      110
Gln Leu Leu Gly Asp Lys Thr Phe
      115      120
<210> 39
<211> 448
<212> DNA
<213> Helicobacter pylori
<220>
<221> CDS
<222> (1)..(447)
<400> 39
ctc ttt gca gat att cca gaa gct tta gaa aac acc caa gaa atc gct 48
Leu Phe Ala Asp Ile Pro Glu Ala Leu Glu Asn Thr Gln Glu Ile Ala
  1      5      10      15
gat aaa tgc gtt tta gag att gat tta aaa gac gat aaa aag aac ccc 96
Asp Lys Cys Val Leu Glu Ile Asp Leu Lys Asp Asp Lys Lys Asn Pro
      20      25      30
cca acc ccc cca agc ttc aaa ttc act aaa gct tac gct caa aat gag 144
Pro Thr Pro Pro Ser Phe Lys Phe Thr Lys Ala Tyr Ala Gln Asn Glu
      35      40      45
ggg ctg aat ttt gaa gat gac gct tct tat ttt gcc tat aag gct aga 192
Gly Leu Asn Phe Glu Asp Asp Ala Ser Tyr Phe Ala Tyr Lys Ala Arg
      50      55      60
gaa ggc ttg aaa gag cgc tta gtt tta gta cca aaa gaa aag cat gat 240

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Glu Gly Leu Lys Glu Arg Leu Val Leu Val Pro Lys Glu Lys His Asp
 65 70 75 80
 caa tat aaa gag cgc cta gaa aaa gaa att gaa gtc att acg aac atg 288
 Gln Tyr Lys Glu Arg Leu Glu Lys Glu Ile Glu Val Ile Thr Asn Met
 85 90 95
 aaa ttc cca ggg tat atg ctg att gtg tgg gat ttt atc cgt tat gct 336
 Lys Phe Pro Gly Tyr Met Leu Ile Val Trp Asp Phe Ile Arg Tyr Ala
 100 105 110
 aag gaa atg ggc att cct gta ggg cct ggt agg ggg agt gcg gcc ggg 384
 Lys Glu Met Gly Ile Pro Val Gly Pro Gly Arg Gly Ser Ala Ala Gly
 115 120 125
 agc ttg gtg gct ttt gct tta aaa atc acg gat att gac cct ttg aaa 432
 Ser Leu Val Ala Phe Ala Leu Lys Ile Thr Asp Ile Asp Pro Leu Lys
 130 135 140
 tac gat ttg ctc ttt g 448
 Tyr Asp Leu Leu Phe
 145
 <210> 40
 <211> 149
 <212> PRT
 <213> *Helicobacter pylori*
 <400> 40
 Leu Phe Ala Asp Ile Pro Glu Ala Leu Glu Asn Thr Gln Glu Ile Ala
 1 5 10 15
 Asp Lys Cys Val Leu Glu Ile Asp Leu Lys Asp Asp Lys Lys Asn Pro
 20 25 30
 Pro Thr Pro Pro Ser Phe Lys Phe Thr Lys Ala Tyr Ala Gln Asn Glu
 35 40 45
 Gly Leu Asn Phe Glu Asp Asp Ala Ser Tyr Phe Ala Tyr Lys Ala Arg
 50 55 60
 Glu Gly Leu Lys Glu Arg Leu Val Leu Val Pro Lys Glu Lys His Asp
 65 70 75 80
 Gln Tyr Lys Glu Arg Leu Glu Lys Glu Ile Glu Val Ile Thr Asn Met
 85 90 95
 Lys Phe Pro Gly Tyr Met Leu Ile Val Trp Asp Phe Ile Arg Tyr Ala
 100 105 110
 Lys Glu Met Gly Ile Pro Val Gly Pro Gly Arg Gly Ser Ala Ala Gly
 115 120 125
 Ser Leu Val Ala Phe Ala Leu Lys Ile Thr Asp Ile Asp Pro Leu Lys
 130 135 140
 Tyr Asp Leu Leu Phe
 145
 <210> 41
 <211> 147
 <212> DNA
 <213> *Helicobacter pylori*
 <220>
 <221> CDS
 <222> (1)..(147)
 <400> 41
 caa tac gac ttt aag gcg atg ttt act ccc ttg atc atg caa gcg cag 48
 Gln Tyr Asp Phe Lys Ala Met Phe Thr Pro Leu Ile Met Gln Ala Gln
 1 5 10 15
 ttg agc tta aga aac att gat aat ttt gtg gaa aaa ggc tct gct ttg 96
 Leu Ser Leu Arg Asn Ile Asp Asn Phe Val Glu Lys Gly Ser Ala Leu
 20 25 30
 ata gat aaa ttt gac gct aac ccc tat aaa acg att ttt gga gaa agg 144
 Ile Asp Lys Phe Asp Ala Asn Pro Tyr Lys Thr Ile Phe Gly Glu Arg
 35 40 45
 aaa
 Lys 147

<210> 42

<211> 49

<212> PRT

<213> Helicobacter pylori

<400> 42

Gln Tyr Asp Phe Lys Ala Met Phe Thr Pro Leu Ile Met Gln Ala Gln
 1 5 10 15
 Leu Ser Leu Arg Asn Ile Asp Asn Phe Val Glu Lys Gly Ser Ala Leu
 20 25 30
 Ile Asp Lys Phe Asp Ala Asn Pro Tyr Lys Thr Ile Phe Gly Glu Arg
 35 40 45
 Lys

<210> 43

<211> 455

<212> DNA

<213> Helicobacter pylori

<220>

<221> CDS

<222> (1)..(453)

<400> 43

aat ttc aat tca gcg aat att act acg agt ttg aat aat tcc tct atc 48
 Asn Phe Asn Ser Ala Asn Ile Thr Thr Ser Leu Asn Asn Ser Ser Ile
 1 5 10 15
 gtg ttt aag ggg gcg gtc tct tta gga ggg cag ttt aat tta agc aat 96
 Val Phe Lys Gly Ala Val Ser Leu Gly Gly Gln Phe Asn Leu Ser Asn
 20 25 30
 aac tct tct tta gat ttc caa ggc tct agc gct atc acc tct aac acg 144
 Asn Ser Ser Leu Asp Phe Gln Gly Ser Ser Ala Ile Thr Ser Asn Thr
 35 40 45
 gcg ttt aat ttc tat gat aac gct ttt tct caa agc ccc atc act ttc 192
 Ala Phe Asn Phe Tyr Asp Asn Ala Phe Ser Gln Ser Pro Ile Thr Phe
 50 55 60
 cat caa gcc ctt gac att aaa gcg ccc tta agt ttg gga ggc aac ctt 240
 His Gln Ala Leu Asp Ile Lys Ala Pro Leu Ser Leu Gly Gly Asn Leu
 65 70 75 80
 tta aac cct aac aac agc agc gtg ctg gat tta aaa aac agc cag ctt 288
 Leu Asn Pro Asn Asn Ser Ser Val Leu Asp Leu Lys Asn Ser Gln Leu
 85 90 95
 gtt ttt ggc gat caa ggg agt ttg aat atc gct aac att gat tta cta 336
 Val Phe Gly Asp Gln Gly Ser Leu Asn Ile Ala Asn Ile Asp Leu Leu
 100 105 110
 agc gat cta aat gat aat aaa aat cgt gtg tat aac atc att caa gcg 384
 Ser Asp Leu Asn Asp Asn Lys Asn Arg Val Tyr Asn Ile Ile Gln Ala
 115 120 125
 gac atg aat agt aat tgg tat gag cgt atc agc ttc ttt ggc atg cac 432
 Asp Met Asn Ser Asn Trp Tyr Glu Arg Ile Ser Phe Phe Gly Met His
 130 135 140
 atc aat gac ggg att tat gat gc 455
 Ile Asn Asp Gly Ile Tyr Asp
 145 150

<210> 44

<211> 151

<212> PRT

<213> Helicobacter pylori

<400> 44

Asn Phe Asn Ser Ala Asn Ile Thr Thr Ser Leu Asn Asn Ser Ser Ile
 1 5 10 15
 Val Phe Lys Gly Ala Val Ser Leu Gly Gly Gln Phe Asn Leu Ser Asn
 20 25 30
 Asn Ser Ser Leu Asp Phe Gln Gly Ser Ser Ala Ile Thr Ser Asn Thr

35 40 45
 Ala Phe Asn Phe Tyr Asp Asn Ala Phe Ser Gln Ser Pro Ile Thr Phe
 50 55 60
 His Gln Ala Leu Asp Ile Lys Ala Pro Leu Ser Leu Gly Gly Asn Leu
 65 70 75 80
 Leu Asn Pro Asn Asn Ser Ser Val Leu Asp Leu Lys Asn Ser Gln Leu
 85 90 95
 Val Phe Gly Asp Gln Gly Ser Leu Asn Ile Ala Asn Ile Asp Leu Leu
 100 105 110
 Ser Asp Leu Asn Asp Asn Lys Asn Arg Val Tyr Asn Ile Ile Gln Ala
 115 120 125
 Asp Met Asn Ser Asn Trp Tyr Glu Arg Ile Ser Phe Phe Gly Met His
 130 135 140
 Ile Asn Asp Gly Ile Tyr Asp
 145 150

<210> 45

<211> 333

<212> DNA

<213> Helicobacter pylori

<220>

<221> CDS

<222> (1)..(333)

<400> 45

gat ttt agt ttc aac gca caa ggc aat gtt ttt gtg caa aat tcc act 48
 Asp Phe Ser Phe Asn Ala Gln Gly Asn Val Phe Val Gln Asn Ser Thr
 1 5 10 15
 ttc tct aac gcc aat gga ggc acg ctc tct ttt aac gca gga aat tcg 96
 Phe Ser Asn Ala Asn Gly Gly Thr Leu Ser Phe Asn Ala Gly Asn Ser
 20 25 30
 ctc att ttt gcc gga aac aat cat att gca ttc act aac cac gct gga 144
 Leu Ile Phe Ala Gly Asn Asn His Ile Ala Phe Thr Asn His Ala Gly
 35 40 45
 act ctt caa tta ttg tcc gat caa gtt tct aac att aac atc acc acg 192
 Thr Leu Gln Leu Leu Ser Asp Gln Val Ser Asn Ile Asn Ile Thr Thr
 50 55 60
 ctt aac gct agc aac ggc ctt aag att aac gcc gct aat aac aat gtt 240
 Leu Asn Ala Ser Asn Gly Leu Lys Ile Asn Ala Ala Asn Asn Asn Val
 65 70 75 80
 tct gtg tct caa ggc aat ctg ttt gtc agc gct agc tgc gcg caa caa 288
 Ser Val Ser Gln Gly Asn Leu Phe Val Ser Ala Ser Cys Ala Gln Gln
 85 90 95
 agc gat cca act aca gct aat att gca aac cct tgc gcg ctt agc 333
 Ser Asp Pro Thr Thr Ala Asn Ile Ala Asn Pro Cys Ala Leu Ser
 100 105 110

<210> 46

<211> 111

<212> PRT

<213> Helicobacter pylori

<400> 46

Asp Phe Ser Phe Asn Ala Gln Gly Asn Val Phe Val Gln Asn Ser Thr
 1 5 10 15
 Phe Ser Asn Ala Asn Gly Gly Thr Leu Ser Phe Asn Ala Gly Asn Ser
 20 25 30
 Leu Ile Phe Ala Gly Asn Asn His Ile Ala Phe Thr Asn His Ala Gly
 35 40 45
 Thr Leu Gln Leu Leu Ser Asp Gln Val Ser Asn Ile Asn Ile Thr Thr
 50 55 60
 Leu Asn Ala Ser Asn Gly Leu Lys Ile Asn Ala Ala Asn Asn Asn Val
 65 70 75 80
 Ser Val Ser Gln Gly Asn Leu Phe Val Ser Ala Ser Cys Ala Gln Gln
 85 90 95

Ser Asp Pro Thr Thr Ala Asn Ile Ala Asn Pro Cys Ala Leu Ser
 100 105 110

<210> 47

<211> 674

<212> DNA

<213> Helicobacter pylori

<220>

<221> CDS

<222> (1)..(672)

<400> 47

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ttg cgc ttg ggc caa ttc aat ggc aat tct ttc aca agc tat aag gat 48
Leu Arg Leu Gly Gln Phe Asn Gly Asn Ser Phe Thr Ser Tyr Lys Asp
  1      5      10      15
agc gct gat cgc acc acg aga gtg gat ttc aac gct aaa aat atc tta 96
Ser Ala Asp Arg Thr Thr Arg Val Asp Phe Asn Ala Lys Asn Ile Leu
      20      25      30
att gat aat ttt tta gaa atc aat aat cgt gtg ggt tct gga gcc ggg 144
Ile Asp Asn Phe Leu Glu Ile Asn Asn Arg Val Gly Ser Gly Ala Gly
      35      40      45
agg aaa gcc agc tct acg gtt tta act ttg caa gct tca gaa ggg att 192
Arg Lys Ala Ser Ser Thr Val Leu Thr Leu Gln Ala Ser Glu Gly Ile
      50      55      60
act agc agt aaa aat gcg gaa att tct ctt tat gat ggc gcc acg ctc 240
Thr Ser Ser Lys Asn Ala Glu Ile Ser Leu Tyr Asp Gly Ala Thr Leu
      65      70      75      80
aat ttg gct tca aac agc gtt aaa tta atg ggt aat gtg tgg atg ggc 288
Asn Leu Ala Ser Asn Ser Val Lys Leu Met Gly Asn Val Trp Met Gly
      85      90      95
cgt ttg caa tat gtg gga gcg tat ttg gcc cct tca tac agc acg ata 336
Arg Leu Gln Tyr Val Gly Ala Tyr Leu Ala Pro Ser Tyr Ser Thr Ile
      100      105      110
aac act tca aaa gtg aca ggg gaa gtg aat ttt aac cat ctc act gtg 384
Asn Thr Ser Lys Val Thr Gly Glu Val Asn Phe Asn His Leu Thr Val
      115      120      125
ggc gat cac aac gcc gct caa gca ggc att atc gct agt aac aag act 432
Gly Asp His Asn Ala Ala Gln Ala Gly Ile Ile Ala Ser Asn Lys Thr
      130      135      140
cat att ggc aca ctg gat ttg tgg caa agc gcg gga cta aac att atc 480
His Ile Gly Thr Leu Asp Leu Trp Gln Ser Ala Gly Leu Asn Ile Ile
      145      150      155      160
gcc cct cca gaa ggc ggt tat aag gat aaa cct aag gat aaa cct agt 528
Ala Pro Pro Glu Gly Tyr Lys Asp Lys Pro Lys Asp Lys Pro Ser
      165      170      175
aac acc acg caa aat aat gct aac aac aac caa caa aac agc gct caa 576
Asn Thr Thr Gln Asn Asn Ala Asn Asn Asn Gln Gln Asn Ser Ala Gln
      180      185      190
aac aat agt aac act cag gtt att aac cca ccc aat agc gcg caa aaa 624
Asn Asn Ser Asn Thr Gln Val Ile Asn Pro Pro Asn Ser Ala Gln Lys
      195      200      205
aca gaa att caa ccc acg caa gtc att gat ggg cct ttt gct ggt ggc 672
Thr Glu Ile Gln Pro Thr Gln Val Ile Asp Gly Pro Phe Ala Gly Gly
      210      215      220
aa

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aa

<210> 48

<211> 224

<212> PRT

<213> Helicobacter pylori

<400> 48

Leu Arg Leu Gly Gln Phe Asn Gly Asn Ser Phe Thr Ser Tyr Lys Asp
 1 5 10 15
 Ser Ala Asp Arg Thr Thr Arg Val Asp Phe Asn Ala Lys Asn Ile Leu

20 25 30
 Ile Asp Asn Phe Leu Glu Ile Asn Asn Arg Val Gly Ser Gly Ala Gly
 35 40 45
 Arg Lys Ala Ser Ser Thr Val Leu Thr Leu Gln Ala Ser Glu Gly Ile
 50 55 60
 Thr Ser Ser Lys Asn Ala Glu Ile Ser Leu Tyr Asp Gly Ala Thr Leu
 65 70 75 80
 Asn Leu Ala Ser Asn Ser Val Lys Leu Met Gly Asn Val Trp Met Gly
 85 90 95
 Arg Leu Gln Tyr Val Gly Ala Tyr Leu Ala Pro Ser Tyr Ser Thr Ile
 100 105 110
 Asn Thr Ser Lys Val Thr Gly Glu Val Asn Phe Asn His Leu Thr Val
 115 120 125
 Gly Asp His Asn Ala Ala Gln Ala Gly Ile Ile Ala Ser Asn Lys Thr
 130 135 140
 His Ile Gly Thr Leu Asp Leu Trp Gln Ser Ala Gly Leu Asn Ile Ile
 145 150 155 160
 Ala Pro Pro Glu Gly Tyr Lys Asp Lys Pro Lys Asp Lys Pro Ser
 165 170 175
 Asn Thr Thr Gln Asn Asn Ala Asn Asn Asn Gln Gln Asn Ser Ala Gln
 180 185 190
 Asn Asn Ser Asn Thr Gln Val Ile Asn Pro Pro Asn Ser Ala Gln Lys
 195 200 205
 Thr Glu Ile Gln Pro Thr Gln Val Ile Asp Gly Pro Phe Ala Gly Gly
 210 215 220

<210> 49

<211> 284

<212> DNA

<213> Helicobacter pylori

<220>

<221> CDS

<222> (1)..(282)

<400> 49

aga ggc ttg cat gat ttt tgg caa aaa ggg tat ttt aac ttt tta agc 48
 Arg Gly Leu His Asp Phe Trp Gln Lys Gly Tyr Phe Asn Phe Leu Ser
 1 5 10 15
 aat ggc tat gtt ttt gtc aat aac agc tct ttt agc aac gct aca gga 96
 Asn Gly Tyr Val Phe Val Asn Asn Ser Ser Phe Ser Asn Ala Thr Gly
 20 25 30
 ggc agt ttg aat ttt gtc gcc aac aag tct att att ttt aat ggc gat 144
 Gly Ser Leu Asn Phe Val Ala Asn Lys Ser Ile Ile Phe Asn Gly Asp
 35 40 45
 aat acg att gac ttt agc aag tat cag ggc gca ttg att ttt gct tct 192
 Asn Thr Ile Asp Phe Ser Lys Tyr Gln Gly Ala Leu Ile Phe Ala Ser
 50 55 60
 aat gat gtt tct aat atc aat atc acc acc cta aac gct act aat ggc 240
 Asn Asp Val Ser Asn Ile Asn Ile Thr Thr Leu Asn Ala Thr Asn Gly
 65 70 75 80
 tta agc ctt aat gcg ggt ttg aat aac gtg agc gtt caa aaa gg 284
 Leu Ser Leu Asn Ala Gly Leu Asn Asn Val Ser Val Gln Lys
 85 90

<210> 50

<211> 94

<212> PRT

<213> Helicobacter pylori

<400> 50

Arg Gly Leu His Asp Phe Trp Gln Lys Gly Tyr Phe Asn Phe Leu Ser
 1 5 10 15
 Asn Gly Tyr Val Phe Val Asn Asn Ser Ser Phe Ser Asn Ala Thr Gly
 20 25 30
 Gly Ser Leu Asn Phe Val Ala Asn Lys Ser Ile Ile Phe Asn Gly Asp

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          35          40          45
Asn Thr Ile Asp Phe Ser Lys Tyr Gln Gly Ala Leu Ile Phe Ala Ser
   50          55          60
Asn Asp Val Ser Asn Ile Asn Ile Thr Thr Leu Asn Ala Thr Asn Gly
   65          70          75          80
Leu Ser Leu Asn Ala Gly Leu Asn Asn Val Ser Val Gln Lys
          85          90

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<210> 51

<211> 498

<212> DNA

<213> *Helicobacter pylori*

<220>

<221> CDS

<222> (1)..(498)

<400> 51

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aaa att tta gtg att caa ggg cct aat tta aac atg tta gga cac aga 48
Lys Ile Leu Val Ile Gln Gly Pro Asn Leu Asn Met Leu Gly His Arg
   1           5           10          15
gac cca agg ctt tat ggt atg gta acc tta gac caa atc cat gaa atc 96
Asp Pro Arg Leu Tyr Gly Met Val Thr Leu Asp Gln Ile His Glu Ile
          20          25          30
atg caa act ttc gtg aaa caa ggc aat tta gat gtg gaa tta gag ttt 144
Met Gln Thr Phe Val Lys Gln Gly Asn Leu Asp Val Glu Leu Glu Phe
          35          40          45
ttt caa act aat ttt gag ggc gaa atc att gat aaa atc caa gag agc 192
Phe Gln Thr Asn Phe Glu Gly Glu Ile Ile Asp Lys Ile Gln Glu Ser
          50          55          60
gtg ggc agc gat tat gaa ggg atc atc att aac cct gga gcg ttt tcg 240
Val Gly Ser Asp Tyr Glu Gly Ile Ile Ile Asn Pro Gly Ala Phe Ser
   65          70          75          80
cac act tct att gcg att gca gat gcg atc atg cta gcg ggc aaa ccc 288
His Thr Ser Ile Ala Ile Ala Asp Ala Ile Met Leu Ala Gly Lys Pro
          85          90          95
gtt att gaa gtg cat ctc act aac att caa gcc aga gag gaa ttc agg 336
Val Ile Glu Val His Leu Thr Asn Ile Gln Ala Arg Glu Glu Phe Arg
          100          105          110
aaa aat tct tac act gga gcg gct tgt gga ggc gtg atc atg gga ttt 384
Lys Asn Ser Tyr Thr Gly Ala Ala Cys Gly Gly Val Ile Met Gly Phe
          115          120          125
ggc ccg ctt ggc tac aac atg gct tta atg gcg atg gtc aat att tta 432
Gly Pro Leu Gly Tyr Asn Met Ala Leu Met Ala Met Val Asn Ile Leu
          130          135          140
gcc gaa atg aaa gcg ttc caa gaa gcc caa aaa aac aac cct aat aac 480
Ala Glu Met Lys Ala Phe Gln Glu Ala Gln Lys Asn Asn Pro Asn Asn
          145          150          155          160
ccc att aac aat caa aaa 498
Pro Ile Asn Asn Gln Lys
          165

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<210> 52

<211> 166

<212> PRT

<213> *Helicobacter pylori*

<400> 52

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Lys Ile Leu Val Ile Gln Gly Pro Asn Leu Asn Met Leu Gly His Arg
   1           5           10          15
Asp Pro Arg Leu Tyr Gly Met Val Thr Leu Asp Gln Ile His Glu Ile
          20          25          30
Met Gln Thr Phe Val Lys Gln Gly Asn Leu Asp Val Glu Leu Glu Phe
          35          40          45
Phe Gln Thr Asn Phe Glu Gly Glu Ile Ile Asp Lys Ile Gln Glu Ser
          50          55          60

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Val Gly Ser Asp Tyr Glu Gly Ile Ile Ile Asn Pro Gly Ala Phe Ser
 65 70 75 80
 His Thr Ser Ile Ala Ile Ala Asp Ala Ile Met Leu Ala Gly Lys Pro
 85 90 95
 Val Ile Glu Val His Leu Thr Asn Ile Gln Ala Arg Glu Glu Phe Arg
 100 105 110
 Lys Asn Ser Tyr Thr Gly Ala Ala Cys Gly Gly Val Ile Met Gly Phe
 115 120 125
 Gly Pro Leu Gly Tyr Asn Met Ala Leu Met Ala Met Val Asn Ile Leu
 130 135 140
 Ala Glu Met Lys Ala Phe Gln Glu Ala Gln Lys Asn Asn Pro Asn Asn
 145 150 155 160
 Pro Ile Asn Asn Gln Lys
 165

<210> 53

<211> 75

<212> DNA

<213> Helicobacter pylori

<220>

<221> CDS

<222> (1)..(75)

<400> 53

caa tct ttg ata aca ata ata aat cgg cta atg caa aaa cag gac cag 48
 Gln Ser Leu Ile Thr Ile Ile Asn Arg Leu Met Gln Lys Gln Asp Gln
 1 5 10 15
 cga cta tca tcg ctc aag gca caa aaa 75
 Arg Leu Ser Ser Leu Lys Ala Gln Lys
 20 25

<210> 54

<211> 25

<212> PRT

<213> Helicobacter pylori

<400> 54

Gln Ser Leu Ile Thr Ile Ile Asn Arg Leu Met Gln Lys Gln Asp Gln
 1 5 10 15
 Arg Leu Ser Ser Leu Lys Ala Gln Lys
 20 25

<210> 55

<211> 679

<212> DNA

<213> Helicobacter pylori

<220>

<221> CDS

<222> (1)..(678)

<400> 55

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 Phe Asn Asn Ser Ala Ser Phe Asn Phe Asn Asn Ser Asn Ala Thr Thr
 1 5 10 15
 tcg ttt gtg ggg gat ttc act aac gct aat tca aat ttg caa atc gcc 96
 Ser Phe Val Gly Asp Phe Thr Asn Ala Asn Ser Asn Leu Gln Ile Ala
 20 25 30
 ggg aac gct gtt ttt ggg aac tct act aat ggc tct caa aat acc gct 144
 Gly Asn Ala Val Phe Gly Asn Ser Thr Asn Gly Ser Gln Asn Thr Ala
 35 40 45
 aat ttt aat aat acc ggc tct gtt aat att tca ggg aat gca acc ttt 192
 Asn Phe Asn Asn Thr Gly Ser Val Asn Ile Ser Gly Asn Ala Thr Phe
 50 55 60
 gat aat gtg gtg ttt aat ggc cct acg aac acg agc gtg aaa ggg cag 240
 Asp Asn Val Val Phe Asn Gly Pro Thr Asn Thr Ser Val Lys Gly Gln
 65 70 75 80
 gtt act tta aat aac atc act tta aaa aac ctg aac gcc cct ttg tct 288

Val Thr Leu Asn Asn Ile Thr Leu Lys Asn Leu Asn Ala Pro Leu Ser
 85 90 95
 ttt ggc gat ggg acg att act ttt aac gct cat tcg gtg att aat att 336
 Phe Gly Asp Gly Thr Ile Thr Phe Asn Ala His Ser Val Ile Asn Ile
 100 105 110
 gct gaa tct atc act aat ggc aac cct atc act ctt gta agc tct tct 384
 Ala Glu Ser Ile Thr Asn Gly Asn Pro Ile Thr Leu Val Ser Ser Ser
 115 120 125
 aaa gaa att gaa tac aac aac gct ttc agt aaa aat cta tgg cag ctc 432
 Lys Glu Ile Glu Tyr Asn Asn Ala Phe Ser Lys Asn Leu Trp Gln Leu
 130 135 140
 atc aac tac caa ggg cat ggg gca agc agt gaa aag ctc gtc tct agc 480
 Ile Asn Tyr Gln Gly His Gly Ala Ser Ser Glu Lys Leu Val Ser Ser
 145 150 155 160
 gcg ggt aat ggc gtt tat gat gtg gtg tat tct ttc aat aac caa acc 528
 Ala Gly Asn Gly Val Tyr Asp Val Val Tyr Ser Phe Asn Asn Gln Thr
 165 170 175
 tac aat ttc caa gag gtt ttt tca caa aac agc att tct atc cgg cgt 576
 Tyr Asn Phe Gln Glu Val Phe Ser Gln Asn Ser Ile Ser Ile Arg Arg
 180 185 190
 ttg ggc gtt aac atg gtg ttt gat tat gtg gat atg gaa aaa tcg gat 624
 Leu Gly Val Asn Met Val Phe Asp Tyr Val Asp Met Glu Lys Ser Asp
 195 200 205
 cat tta tat tat caa aac gct ctc ggt ttt atg acc tac atg cct aat 672
 His Leu Tyr Tyr Gln Asn Ala Leu Gly Phe Met Thr Tyr Met Pro Asn
 210 215 220
 agc tat a 679
 Ser Tyr
 225
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 <213> *Helicobacter pylori*
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 Gly Asn Ala Val Phe Gly Asn Ser Thr Asn Gly Ser Gln Asn Thr Ala
 35 40 45
 Asn Phe Asn Asn Thr Gly Ser Val Asn Ile Ser Gly Asn Ala Thr Phe
 50 55 60
 Asp Asn Val Val Phe Asn Gly Pro Thr Asn Thr Ser Val Lys Gly Gln
 65 70 75 80
 Val Thr Leu Asn Asn Ile Thr Leu Lys Asn Leu Asn Ala Pro Leu Ser
 85 90 95
 Phe Gly Asp Gly Thr Ile Thr Phe Asn Ala His Ser Val Ile Asn Ile
 100 105 110
 Ala Glu Ser Ile Thr Asn Gly Asn Pro Ile Thr Leu Val Ser Ser Ser
 115 120 125
 Lys Glu Ile Glu Tyr Asn Asn Ala Phe Ser Lys Asn Leu Trp Gln Leu
 130 135 140
 Ile Asn Tyr Gln Gly His Gly Ala Ser Ser Glu Lys Leu Val Ser Ser
 145 150 155 160
 Ala Gly Asn Gly Val Tyr Asp Val Val Tyr Ser Phe Asn Asn Gln Thr
 165 170 175
 Tyr Asn Phe Gln Glu Val Phe Ser Gln Asn Ser Ile Ser Ile Arg Arg
 180 185 190
 Leu Gly Val Asn Met Val Phe Asp Tyr Val Asp Met Glu Lys Ser Asp
 195 200 205
 His Leu Tyr Tyr Gln Asn Ala Leu Gly Phe Met Thr Tyr Met Pro Asn

210
 Ser Tyr
 225
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 <211> 750
 <212> DNA
 <213> *Helicobacter pylori*
 <220>
 <221> CDS
 <222> (1)..(750)
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 1 5 10 15
 cac ctt aat ttt aac ggg gcg gtt aat ttc aat tca gcg aat att act 96
 His Leu Asn Phe Asn Gly Ala Val Asn Phe Asn Ser Ala Asn Ile Thr
 20 25 30
 acg agt ttg aat aat tcc tct atc gtg ttt aag ggg gcg gtc tct tta 144
 Thr Ser Leu Asn Asn Ser Ser Ile Val Phe Lys Gly Ala Val Ser Leu
 35 40 45
 gga ggg cag ttt aat tta agc aat aac tct tct tta gat ttc caa ggc 192
 Gly Gly Gln Phe Asn Leu Ser Asn Asn Ser Ser Leu Asp Phe Gln Gly
 50 55 60
 tct agc gct atc acc tct aac acg gcg ttt aat ttc tat gat aac gct 240
 Ser Ser Ala Ile Thr Ser Asn Thr Ala Phe Asn Phe Tyr Asp Asn Ala
 65 70 75 80
 ttt tct caa agc ccc atc act ttc cat caa gcc ctt gac att aaa gcg 288
 Phe Ser Gln Ser Pro Ile Thr Phe His Gln Ala Leu Asp Ile Lys Ala
 85 90 95
 ccc tta agt ttg gga ggc aac ctt tta aac cct aac aac agc agc gtg 336
 Pro Leu Ser Leu Gly Gly Asn Leu Leu Asn Pro Asn Asn Ser Ser Val
 100 105 110
 ctg gat tta aaa aac agc cag ctt gtt ttt ggc gat caa ggg agt ttg 384
 Leu Asp Leu Lys Asn Ser Gln Leu Val Phe Gly Asp Gln Gly Ser Leu
 115 120 125
 aat atc gct aac att gat tta cta agc gat cta aat gat aat aaa aat 432
 Asn Ile Ala Asn Ile Asp Leu Leu Ser Asp Leu Asn Asp Asn Lys Asn
 130 135 140
 cgt gtg tat aac atc att caa gcg gac atg aat agt aat tgg tat gag 480
 Arg Val Tyr Asn Ile Ile Gln Ala Asp Met Asn Ser Asn Trp Tyr Glu
 145 150 155 160
 cgt atc agc ttc ttt ggc atg cac atc aat gac ggg att tat gat gct 528
 Arg Ile Ser Phe Phe Gly Met His Ile Asn Asp Gly Ile Tyr Asp Ala
 165 170 175
 aaa aac caa act tat agt ttc act aac ccc ctt aat aac gcc cta aaa 576
 Lys Asn Gln Thr Tyr Ser Phe Thr Asn Pro Leu Asn Asn Ala Leu Lys
 180 185 190
 atc acc gag agc ttt aaa gac aac caa cta agc gtt acg ctc tct caa 624
 Ile Thr Glu Ser Phe Lys Asp Asn Gln Leu Ser Val Thr Leu Ser Gln
 195 200 205
 atc ccg ggt att aaa aac acg ctc tat aac att ggc tct gaa att ttt 672
 Ile Pro Gly Ile Lys Asn Thr Leu Tyr Asn Ile Gly Ser Glu Ile Phe
 210 215 220
 aac tac caa aaa gtt tat aac aac gct aat ggc gtg tat tct tat agc 720
 Asn Tyr Gln Lys Val Tyr Asn Asn Ala Asn Gly Val Tyr Ser Tyr Ser
 225 230 235 240
 gat gat gca caa ggc gtg ttt tat ctc aca 750
 Asp Asp Ala Gln Gly Val Phe Tyr Leu Thr
 245 250
 <210> 58
 <211> 250

<212> PRT

<213> Helicobacter pylori

<400> 58

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Asn Ala Thr Ile Asn Asp Tyr Ala Ser Leu Ile Ala Ser Asn Gly Ser
 1           5           10           15
His Leu Asn Phe Asn Gly Ala Val Asn Phe Asn Ser Ala Asn Ile Thr
          20           25           30
Thr Ser Leu Asn Asn Ser Ser Ile Val Phe Lys Gly Ala Val Ser Leu
          35           40           45
Gly Gly Gln Phe Asn Leu Ser Asn Asn Ser Ser Leu Asp Phe Gln Gly
          50           55           60
Ser Ser Ala Ile Thr Ser Asn Thr Ala Phe Asn Phe Tyr Asp Asn Ala
          65           70           75           80
Phe Ser Gln Ser Pro Ile Thr Phe His Gln Ala Leu Asp Ile Lys Ala
          85           90           95
Pro Leu Ser Leu Gly Gly Asn Leu Leu Asn Pro Asn Asn Ser Ser Val
          100          105          110
Leu Asp Leu Lys Asn Ser Gln Leu Val Phe Gly Asp Gln Gly Ser Leu
          115          120          125
Asn Ile Ala Asn Ile Asp Leu Leu Ser Asp Leu Asn Asp Asn Lys Asn
          130          135          140
Arg Val Tyr Asn Ile Ile Gln Ala Asp Met Asn Ser Asn Trp Tyr Glu
          145          150          155          160
Arg Ile Ser Phe Phe Gly Met His Ile Asn Asp Gly Ile Tyr Asp Ala
          165          170          175
Lys Asn Gln Thr Tyr Ser Phe Thr Asn Pro Leu Asn Asn Ala Leu Lys
          180          185          190
Ile Thr Glu Ser Phe Lys Asp Asn Gln Leu Ser Val Thr Leu Ser Gln
          195          200          205
Ile Pro Gly Ile Lys Asn Thr Leu Tyr Asn Ile Gly Ser Glu Ile Phe
          210          215          220
Asn Tyr Gln Lys Val Tyr Asn Asn Ala Asn Gly Val Tyr Ser Tyr Ser
          225          230          235          240
Asp Asp Ala Gln Gly Val Phe Tyr Leu Thr
          245          250

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<210> 59

<211> 989

<212> DNA

<213> Helicobacter pylori

<220>

<221> CDS

<222> (1)..(987)

<400> 59

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 1           5           10           15
tta agg gct aaa aat atc cat atc aat ttc caa ggc gtt tct act ttt 96
Leu Arg Ala Lys Asn Ile His Ile Asn Phe Gln Gly Val Ser Thr Phe
          20           25           30
aaa caa aac tct acg atg aat tta gct gaa agt tcc caa gcg agc ttt 144
Lys Gln Asn Ser Thr Met Asn Leu Ala Glu Ser Ser Gln Ala Ser Phe
          35           40           45
aac gct ctt aaa gtg gaa ggg gaa acg aat ttc aat ctc aat aac tca 192
Asn Ala Leu Lys Val Glu Gly Glu Thr Asn Phe Asn Leu Asn Asn Ser
          50           55           60
agc ttg ttg aat ttc aat ggc aat agc gtt ttc aac gct cct gtg agt 240
Ser Leu Leu Asn Phe Asn Gly Asn Ser Val Phe Asn Ala Pro Val Ser
          65           70           75           80
ttt tat gct aat cat tct caa att tct ttc act aaa tta gcg act ttt 288
Phe Tyr Ala Asn His Ser Gln Ile Ser Phe Thr Lys Leu Ala Thr Phe
          85           90           95

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aat tct gac gct tct ttt gat tta agc aac aac agc acc ctg aat ttt 336
 Asn Ser Asp Ala Ser Phe Asp Leu Ser Asn Asn Ser Thr Leu Asn Phe
 100 105 110
 caa agc gtt ctt tta aat ggt gct cta aac ctt tta ggc aat ggc agt 384
 Gln Ser Val Leu Leu Asn Gly Ala Leu Asn Leu Leu Gly Asn Gly Ser
 115 120 125
 aac aat cta gcg atc aac gct aaa ggg aat ttt agt ttt ggg tct aaa 432
 Asn Asn Leu Ala Ile Asn Ala Lys Gly Asn Phe Ser Phe Gly Ser Lys
 130 135 140
 ggg att ttg aat ctg tct tat atg aat cta ttt ggg ggg gat aaa aaa 480
 Gly Ile Leu Asn Leu Ser Tyr Met Asn Leu Phe Gly Gly Asp Lys Lys
 145 150 155 160
 act tcc gtt tat gat gtg ttg caa gcc caa aat att gat ggc tta atg 528
 Thr Ser Val Tyr Asp Val Leu Gln Ala Gln Asn Ile Asp Gly Leu Met
 165 170 175
 ggg aat aac ggc tat gag aag atc cgt ttt tat ggc ata cag att gac 576
 Gly Asn Asn Gly Tyr Glu Lys Ile Arg Phe Tyr Gly Ile Gln Ile Asp
 180 185 190
 aag gct gat tac tcg ttt gat aac ggc gtt cat tct tgg aga ttc act 624
 Lys Ala Asp Tyr Ser Phe Asp Asn Gly Val His Ser Trp Arg Phe Thr
 195 200 205
 aac ccg ctc aat acg act gaa acg att aca gaa acc ttg cat aac aac 672
 Asn Pro Leu Asn Thr Thr Glu Thr Ile Thr Glu Thr Leu His Asn Asn
 210 215 220
 cgc ttg aaa gtg cag atc tct caa aac ggc gtt tct aat aat aag atg 720
 Arg Leu Lys Val Gln Ile Ser Gln Asn Gly Val Ser Asn Asn Lys Met
 225 230 235 240
 ttc aat ctc gct cct agc ttg tat gat tac caa aaa aac cct tat aat 768
 Phe Asn Leu Ala Pro Ser Leu Tyr Asp Tyr Gln Lys Asn Pro Tyr Asn
 245 250 255
 gaa acc gag aat tcc tat aat tac aca agc gat aag gtt ggc act tat 816
 Glu Thr Glu Asn Ser Tyr Asn Tyr Thr Ser Asp Lys Val Gly Thr Tyr
 260 265 270
 tat tta acg agc aat atc aaa ggc ttt aat caa aac aat aaa aca ccc 864
 Tyr Leu Thr Ser Asn Ile Lys Gly Phe Asn Gln Asn Asn Lys Thr Pro
 275 280 285
 ggg act tat aac gcg caa aac caa ccc tta caa gcc tta cac att tac 912
 Gly Thr Tyr Asn Ala Gln Asn Gln Pro Leu Gln Ala Leu His Ile Tyr
 290 295 300
 aat cag gct atc act aag caa gat ttg aac atg atc gcc agt ttg ggt 960
 Asn Gln Ala Ile Thr Lys Gln Asp Leu Asn Met Ile Ala Ser Leu Gly
 305 310 315 320
 aag gag ttt ttg cct aaa ata gcc aat ct 989
 Lys Glu Phe Leu Pro Lys Ile Ala Asn
 325

<210> 60

<211> 329

<212> PRT

<213> Helicobacter pylori

<400> 60

Leu Ile Asn Phe Lys Gly Asn Thr Asn Phe Asn Gln Ala Thr Leu Asn
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 Leu Arg Ala Lys Asn Ile His Ile Asn Phe Gln Gly Val Ser Thr Phe
 20 25 30
 Lys Gln Asn Ser Thr Met Asn Leu Ala Glu Ser Ser Gln Ala Ser Phe
 35 40 45
 Asn Ala Leu Lys Val Glu Gly Glu Thr Asn Phe Asn Leu Asn Asn Ser
 50 55 60
 Ser Leu Leu Asn Phe Asn Gly Asn Ser Val Phe Asn Ala Pro Val Ser
 65 70 75 80
 Phe Tyr Ala Asn His Ser Gln Ile Ser Phe Thr Lys Leu Ala Thr Phe

85										90				95			
Asn	Ser	Asp	Ala	Ser	Phe	Asp	Leu	Ser	Asn	Asn	Ser	Thr	Leu	Asn	Phe		
100								105				110					
Gln	Ser	Val	Leu	Leu	Asn	Gly	Ala	Leu	Asn	Leu	Leu	Gly	Asn	Gly	Ser		
115								120				125					
Asn	Asn	Leu	Ala	Ile	Asn	Ala	Lys	Gly	Asn	Phe	Ser	Phe	Gly	Ser	Lys		
130								135				140					
Gly	Ile	Leu	Asn	Leu	Ser	Tyr	Met	Asn	Leu	Phe	Gly	Gly	Asp	Lys	Lys		
145				150				155				160					
Thr	Ser	Val	Tyr	Asp	Val	Leu	Gln	Ala	Gln	Asn	Ile	Asp	Gly	Leu	Met		
				165				170				175					
Gly	Asn	Asn	Gly	Tyr	Glu	Lys	Ile	Arg	Phe	Tyr	Gly	Ile	Gln	Ile	Asp		
180								185				190					
Lys	Ala	Asp	Tyr	Ser	Phe	Asp	Asn	Gly	Val	His	Ser	Trp	Arg	Phe	Thr		
195								200				205					
Asn	Pro	Leu	Asn	Thr	Thr	Glu	Thr	Ile	Thr	Glu	Thr	Leu	His	Asn	Asn		
210				215				220									
Arg	Leu	Lys	Val	Gln	Ile	Ser	Gln	Asn	Gly	Val	Ser	Asn	Asn	Lys	Met		
225				230				235				240					
Phe	Asn	Leu	Ala	Pro	Ser	Leu	Tyr	Asp	Tyr	Gln	Lys	Asn	Pro	Tyr	Asn		
				245				250				255					
Glu	Thr	Glu	Asn	Ser	Tyr	Asn	Tyr	Thr	Ser	Asp	Lys	Val	Gly	Thr	Tyr		
260								265				270					
Tyr	Leu	Thr	Ser	Asn	Ile	Lys	Gly	Phe	Asn	Gln	Asn	Asn	Lys	Thr	Pro		
275								280				285					
Gly	Thr	Tyr	Asn	Ala	Gln	Asn	Gln	Pro	Leu	Gln	Ala	Leu	His	Ile	Tyr		
290				295				300									
Asn	Gln	Ala	Ile	Thr	Lys	Gln	Asp	Leu	Asn	Met	Ile	Ala	Ser	Leu	Gly		
305				310				315				320					
Lys	Glu	Phe	Leu	Pro	Lys	Ile	Ala	Asn									
				325													

<210> 61

<211> 357

<212> DNA

<213> *Helicobacter pylori*

<220>

<221> CDS

<222> (1) . . (357)

<400> 61

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Leu Met Leu Lys Asp Thr His Leu Arg His Val Lys Asp Leu Lys Ser
1 5 10 15

ttt tta acg cat gcc aga aaa aac ttg cct ttc acg gct aaa att gaa 96
Phe Leu Thr His Ala Arg Lys Asn Leu Pro Phe Thr Ala Lys Ile Glu
20 25 30

att gaa tgc gaa agc ttt gaa gag gcc aaa aac gcc atg aat gcg gga 144
Ile Glu Cys Glu Ser Phe Glu Glu Ala Lys Asn Ala Met Asn Ala Gly

gcg gat att gtg atg tgc gat aat ttg agc gtt tta gag act aaa gaa 192
Ala Asp Ile Val Met Cys Asp Asn Leu Ser Val Leu Glu Thr Lys Glu

att gcc gct tat aga gat gcg cat tat ccc ttt gtt tta ctg gaa gcg 240
Ile Ala Ala Tyr Arg Asp Ala His Tyr Pro Phe Val Leu Leu Glu Ala

65 70 75 80 288
 agc ggg aac att tca cta gag agc att aac gct tac gct aaa agc ggc
 Ser Gly Asn Ile Ser Leu Glu Ser Ile Asn Ala Tyr Ala Lys Ser Gly

gtg gat gcc att agc gta ggg gct tta atc cat caa gcc act ttt att 336
Val Asp Ala Ile Ser Val Gly Ala Leu Ile His Gln Ala Thr Phe Ile

100 105 110 357

gac atg cac atg aaa atg gct

357

Asp Met His Met Lys Met Ala

115

<210> 62

<211> 119

<212> PRT

<213> Helicobacter pylori

<400> 62

Leu Met Leu Lys Asp Thr His Leu Arg His Val Lys Asp Leu Lys Ser
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 Phe Leu Thr His Ala Arg Lys Asn Leu Pro Phe Thr Ala Lys Ile Glu
 20 25 30
 Ile Glu Cys Glu Ser Phe Glu Glu Ala Lys Asn Ala Met Asn Ala Gly
 35 40 45
 Ala Asp Ile Val Met Cys Asp Asn Leu Ser Val Leu Glu Thr Lys Glu
 50 55 60
 Ile Ala Ala Tyr Arg Asp Ala His Tyr Pro Phe Val Leu Leu Glu Ala
 65 70 75 80
 Ser Gly Asn Ile Ser Leu Glu Ser Ile Asn Ala Tyr Ala Lys Ser Gly
 85 90 95
 Val Asp Ala Ile Ser Val Gly Ala Leu Ile His Gln Ala Thr Phe Ile
 100 105 110

Asp Met His Met Lys Met Ala

115

<210> 63

<211> 437

<212> DNA

<213> Helicobacter pylori

<220>

<221> CDS

<222> (1)..(435)

<400> 63

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 1 5 10 15
 gtg gat ttg gaa tgg ttt gaa acg agg aaa atc gct cgt ttt aaa 96
 Val Asp Leu Glu Trp Phe Glu Thr Arg Lys Lys Ile Ala Arg Phe Lys
 20 25 30
 acc agg caa ggc aaa gac ata gcc ata cgc ctt aaa gac gct ccc aag 144
 Thr Arg Gln Gly Lys Asp Ile Ala Ile Arg Leu Lys Asp Ala Pro Lys
 35 40 45
 ttg ggg ctc tct caa ggg gat att tta ttt aaa gaa gag aag gaa att 192
 Leu Gly Leu Ser Gln Gly Asp Ile Leu Phe Lys Glu Glu Lys Glu Ile
 50 55 60
 atc gcc gtt aat atc ttg gat tct gaa gtc att cac atc caa gcc aag 240
 Ile Ala Val Asn Ile Leu Asp Ser Glu Val Ile His Ile Gln Ala Lys
 65 70 75 80
 agc gtg gca gaa gta gcg aaa ata tgc tat gaa ata gga aac cgc cat 288
 Ser Val Ala Glu Val Ala Lys Ile Cys Tyr Glu Ile Gly Asn Arg His
 85 90 95
 gcg gct tta tac tat ggc gag tct caa ttt gaa ttt aaa aca cca ttt 336
 Ala Ala Leu Tyr Tyr Gly Glu Ser Gln Phe Glu Phe Lys Thr Pro Phe
 100 105 110
 gaa aag ccc acg cta gcg tta tta gaa aag cta ggg gtt caa aat cgt 384
 Glu Lys Pro Thr Leu Ala Leu Leu Glu Lys Leu Gly Val Gln Asn Arg
 115 120 125
 gtt tta agt tca aaa ttg gat tcc aaa gaa cgc tta acc gtg agc atg 432
 Val Leu Ser Ser Lys Leu Asp Ser Lys Glu Arg Leu Thr Val Ser Met
 130 135 140
 ccc ca 437
 Pro
 145

<210> 64

<211> 145

<212> PRT

<213> Helicobacter pylori

<400> 64

Val	Gly	Asn	Leu	Arg	Asp	Leu	Asn	Pro	Leu	Asp	Phe	Ser	Val	Asp	His	
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Val	Asp	Leu	Glu	Trp	Phe	Glu	Thr	Arg	Lys	Lys	Ile	Ala	Arg	Phe	Lys	
		20						25					30			
Thr	Arg	Gln	Gly	Lys	Asp	Ile	Ala	Ile	Arg	Leu	Lys	Asp	Ala	Pro	Lys	
		35				40						45				
Leu	Gly	Leu	Ser	Gln	Gly	Asp	Ile	Leu	Phe	Lys	Glu	Glu	Lys	Glu	Ile	
	50				55					60						
Ile	Ala	Val	Asn	Ile	Leu	Asp	Ser	Glu	Val	Ile	His	Ile	Gln	Ala	Lys	
	65			70					75						80	
Ser	Val	Ala	Glu	Val	Ala	Lys	Ile	Cys	Tyr	Glu	Ile	Gly	Asn	Arg	His	
			85					90					95			
Ala	Ala	Leu	Tyr	Tyr	Gly	Glu	Ser	Gln	Phe	Glu	Phe	Lys	Thr	Pro	Phe	
		100					105						110			
Glu	Lys	Pro	Thr	Leu	Ala	Leu	Leu	Glu	Lys	Leu	Gly	Val	Gln	Asn	Arg	
	115					120					125					
Val	Leu	Ser	Ser	Lys	Leu	Asp	Ser	Lys	Glu	Arg	Leu	Thr	Val	Ser	Met	Pro
	130				135						140				145	

<210> 65

<211> 831

<212> DNA

<213> Helicobacter pylori

<220>

<221> CDS

<222> (1)..(831)

<400> 65

agc	act	ggt	gat	gtt	agt	gaa	caa	ata	gaa	cta	gaa	caa	gaa	aaa	caa	48
Ser	Thr	Gly	Asp	Val	Ser	Glu	Gln	Ile	Glu	Leu	Glu	Gln	Glu	Lys	Gln	
1				5					10					15		
aag	acg	agc	aat	ata	gag	act	aac	aat	caa	ata	aaa	gta	gaa	caa	gaa	96
Lys	Thr	Ser	Asn	Ile	Glu	Thr	Asn	Asn	Gln	Ile	Lys	Val	Glu	Gln	Glu	
		20					25					30				
aaa	caa	aag	aca	agc	aat	ata	gag	act	aat	aat	caa	ata	aaa	gta	gaa	144
Lys	Gln	Lys	Thr	Ser	Asn	Ile	Glu	Thr	Asn	Asn	Gln	Ile	Lys	Val	Glu	
	35				40				45							
caa	gaa	caa	caa	aag	aca	agc	aat	aca	cag	aaa	gat	ttg	gtt	aaa	gaa	192
Gln	Glu	Gln	Gln	Lys	Thr	Ser	Asn	Thr	Gln	Lys	Asp	Leu	Val	Lys	Glu	
	50				55				60							
cag	aaa	gat	ttg	gtt	aaa	gaa	cag	aaa	gat	ttg	gtt	aaa	gaa	cag	aaa	240
Gln	Lys	Asp	Leu	Val	Lys	Glu	Gln	Lys	Asp	Leu	Val	Lys	Glu	Gln	Lys	
	65			70				75					80			
gat	ttg	gtt	aaa	gaa	cag	aaa	gat	ttg	gtt	aaa	aca	cag	aaa	gat	ttc	288
Asp	Leu	Val	Lys	Glu	Gln	Lys	Asp	Leu	Val	Lys	Thr	Gln	Lys	Asp	Phe	
		85					90					95				
att	aaa	tat	gta	gaa	caa	aat	tgc	caa	gaa	aat	cat	aat	caa	ttc	ttt	336
Ile	Lys	Tyr	Val	Glu	Gln	Asn	Cys	Gln	Glu	Asn	His	Asn	Gln	Phe	Phe	
		100				105						110				
att	gaa	aaa	gga	gga	att	aag	gct	ggt	att	ggt	ata	gaa	gta	gaa	gct	384
Ile	Glu	Lys	Gly	Gly	Ile	Lys	Ala	Gly	Ile	Gly	Ile	Glu	Val	Glu	Ala	
	115					120					125					
gaa	tgc	aaa	acc	cct	aaa	cct	gca	aaa	acc	aat	caa	acc	cct	atc	cag	432
Glu	Cys	Lys	Thr	Pro	Lys	Pro	Ala	Lys	Thr	Asn	Gln	Thr	Pro	Ile	Gln	
	130				135						140					
cca	aaa	cac	ctc	cca	aac	tct	aaa	caa	ccc	cgc	tct	caa	aga	gga	tca	480
Pro	Lys	His	Leu	Pro	Asn	Ser	Lys	Gln	Pro	Arg	Ser	Gln	Arg	Gly	Ser	
	145				150				155					160		

aaa gcg caa gag ctt atc gct tat ttg caa aaa gag cta gaa ttt ctg 528
 Lys Ala Gln Glu Leu Ile Ala Tyr Leu Gln Lys Glu Leu Glu Phe Leu
 165 170 175
 ccc tat tcg caa aaa gct atc gct aaa caa gtg gat ttt tac agg cca 576
 Pro Tyr Ser Gln Lys Ala Ile Ala Lys Gln Val Asp Phe Tyr Arg Pro
 180 185 190
 agt tct atc gct tat tta gaa cta gat cct aga gat ttt aag gtt aca 624
 Ser Ser Ile Ala Tyr Leu Glu Leu Asp Pro Arg Asp Phe Lys Val Thr
 195 200 205
 gaa gaa tgg caa aaa gaa aat cta aaa ata cgc tct aaa gct caa gct 672
 Glu Glu Trp Gln Lys Glu Asn Leu Lys Ile Arg Ser Lys Ala Gln Ala
 210 215 220
 aaa atg ctt gaa atg aga aac cca caa gcc cac ctt tca aac tct caa 720
 Lys Met Leu Glu Met Arg Asn Pro Gln Ala His Leu Ser Asn Ser Gln
 225 230 235 240
 agc ctt ttg ttc gtt caa aaa ata ttt gct gat gtt aat aaa gaa ata 768
 Ser Leu Leu Phe Val Gln Lys Ile Phe Ala Asp Val Asn Lys Glu Ile
 245 250 255
 gaa gca gtt gct aat act gaa aag aaa gca gaa aaa gcg ggt tat ggt 816
 Glu Ala Val Ala Asn Thr Glu Lys Lys Ala Glu Lys Ala Gly Tyr Gly
 260 265 270
 tat agt aaa agg atg 831
 Tyr Ser Lys Arg Met
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<210> 66

<211> 277

<212> PRT

<213> Helicobacter pylori

<400> 66

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 20 25 30
 Lys Gln Lys Thr Ser Asn Ile Glu Thr Asn Asn Gln Ile Lys Val Glu
 35 40 45
 Gln Glu Gln Gln Lys Thr Ser Asn Thr Gln Lys Asp Leu Val Lys Glu
 50 55 60
 Gln Lys Asp Leu Val Lys Glu Gln Lys Asp Leu Val Lys Glu Gln Lys
 65 70 75 80
 Asp Leu Val Lys Glu Gln Lys Asp Leu Val Lys Thr Gln Lys Asp Phe
 85 90 95
 Ile Lys Tyr Val Glu Gln Asn Cys Gln Glu Asn His Asn Gln Phe Phe
 100 105 110
 Ile Glu Lys Gly Gly Ile Lys Ala Gly Ile Gly Ile Glu Val Glu Ala
 115 120 125
 Glu Cys Lys Thr Pro Lys Pro Ala Lys Thr Asn Gln Thr Pro Ile Gln
 130 135 140
 Pro Lys His Leu Pro Asn Ser Lys Gln Pro Arg Ser Gln Arg Gly Ser
 145 150 155 160
 Lys Ala Gln Glu Leu Ile Ala Tyr Leu Gln Lys Glu Leu Glu Phe Leu
 165 170 175
 Pro Tyr Ser Gln Lys Ala Ile Ala Lys Gln Val Asp Phe Tyr Arg Pro
 180 185 190
 Ser Ser Ile Ala Tyr Leu Glu Leu Asp Pro Arg Asp Phe Lys Val Thr
 195 200 205
 Glu Glu Trp Gln Lys Glu Asn Leu Lys Ile Arg Ser Lys Ala Gln Ala
 210 215 220
 Lys Met Leu Glu Met Arg Asn Pro Gln Ala His Leu Ser Asn Ser Gln
 225 230 235 240
 Ser Leu Leu Phe Val Gln Lys Ile Phe Ala Asp Val Asn Lys Glu Ile
 245 250 255

Glu Ala Val Ala Asn Thr Glu Lys Lys Ala Glu Lys Ala Gly Tyr Gly
 260 265 270

Tyr Ser Lys Arg Met
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<210> 67

<211> 915

<212> DNA

<213> *Helicobacter pylori*

<220>

<221> CDS

<222> (1)..(915)

<400> 67

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1 5 10 15	
agt ggg gaa tat tgc gtg agc acg gat agt ttt gtc atc acg ccc tta	96
Ser Gly Glu Tyr Cys Val Ser Thr Asp Ser Phe Val Ile Thr Pro Leu	
20 25 30	
att ttt aat ggg ggc gat ata ggc aag ctt tgc gtt tgc ggg agt gcg	144
Ile Phe Asn Gly Gly Asp Ile Gly Lys Leu Cys Val Cys Gly Ser Ala	
35 40 45	
aat gat gtg agc gtg caa ggg ggc gaa cct ttg tat ttg aat atg ggt	192
Asn Asp Val Ser Val Gln Gly Gly Glu Pro Leu Tyr Leu Asn Met Gly	
50 55 60	
ttt att tta gaa gaa ggc tta gaa att tct ctt tta aaa caa att tta	240
Phe Ile Leu Glu Glu Gly Leu Glu Ile Ser Leu Leu Lys Gln Ile Leu	
65 70 75 80	
caa tcc ata caa aaa gaa ttg ttt aaa gcc aac ctg aaa ctc ctc tcc	288
Gln Ser Ile Gln Lys Glu Leu Phe Lys Ala Asn Leu Lys Leu Leu Ser	
85 90 95	
cta gac act aaa gtc gtg cca aag ggg agc gtg gat aag ctt ttt atc	336
Leu Asp Thr Lys Val Val Pro Lys Gly Ser Val Asp Lys Leu Phe Ile	
100 105 110	
aac aca acc tgc att ggt aaa atc atc aag cca ggg att tct tcg tac	384
Asn Thr Thr Cys Ile Gly Lys Ile Ile Lys Pro Gly Ile Ser Ser Tyr	
115 120 125	
cat tta caa caa ggg caa gcc att atc cta agc gac act atc gcc aat	432
His Leu Gln Gln Gly Gln Ala Ile Ile Leu Ser Asp Thr Ile Ala Asn	
130 135 140	
cat ggg gca agc tta ttt gcg atg cgt aat gaa atc aag ctt aaa acg	480
His Gly Ala Ser Leu Phe Ala Met Arg Asn Glu Ile Lys Leu Lys Thr	
145 150 155 160	
aat cta gaa agc gat tgc caa ctg ctc tat ccc tta tta aaa ccc cta	528
Asn Leu Glu Ser Asp Cys Gln Leu Leu Tyr Pro Leu Leu Lys Pro Leu	
165 170 175	
ttt tta agc gat ctc aaa att gat gct tta aga gat gcg act agg ggc	576
Phe Leu Ser Asp Leu Lys Ile Asp Ala Leu Arg Asp Ala Thr Arg Gly	
180 185 190	
ggg tta gcg agc gtg ctg aac gaa tgg gcg aac agc tct aga gtg aaa	624
Gly Leu Ala Ser Val Leu Asn Glu Trp Ala Asn Ser Ser Arg Val Lys	
195 200 205	
atc gtt ata gaa gaa gaa aaa atc ccc tta aaa gaa gaa acg aaa ggg	672
Ile Val Ile Glu Glu Glu Lys Ile Pro Leu Lys Glu Glu Thr Lys Gly	
210 215 220	
att tgt gag att tta ggg tta gaa ccc tac gcg cta gcc aat gag ggg	720
Ile Cys Glu Ile Leu Gly Leu Glu Pro Tyr Ala Leu Ala Asn Glu Gly	
225 230 235 240	
gtg ttt gtt tta gcg ctc aat caa aaa gac gcc cct aaa gcc tta gaa	768
Val Phe Val Leu Ala Leu Asn Gln Lys Asp Ala Pro Lys Ala Leu Glu	
245 250 255	
att tta aaa agt aac gaa aaa gct aaa aac gct tgc gtg att ggc aaa	816

Ile Leu Lys Ser Asn Glu Lys Ala Lys Asn Ala Cys Val Ile Gly Lys
 260 265 270
 gtg ttt gaa aac cct tat cct agc gtg gtt tta aag aac gca tgg ggt 864
 Val Phe Glu Asn Pro Tyr Pro Ser Val Val Leu Lys Asn Ala Trp Gly
 275 280 285
 ttt gaa agg att tta gag gtg cca gag ggc gaa tta ttg cct agg att 912
 Phe Glu Arg Ile Leu Glu Val Pro Glu Gly Glu Leu Leu Pro Arg Ile
 290 295 300
 915

tgt

Cys

305

<210> 68

<211> 305

<212> PRT

<213> Helicobacter pylori

<400> 68

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 Ser Gly Glu Tyr Cys Val Ser Thr Asp Ser Phe Val Ile Thr Pro Leu
 20 25 30
 Ile Phe Asn Gly Gly Asp Ile Gly Lys Leu Cys Val Cys Gly Ser Ala
 35 40 45
 Asn Asp Val Ser Val Gln Gly Gly Glu Pro Leu Tyr Leu Asn Met Gly
 50 55 60
 Phe Ile Leu Glu Glu Gly Leu Glu Ile Ser Leu Leu Lys Gln Ile Leu
 65 70 75 80
 Gln Ser Ile Gln Lys Glu Leu Phe Lys Ala Asn Leu Lys Leu Leu Ser
 85 90 95
 Leu Asp Thr Lys Val Val Pro Lys Gly Ser Val Asp Lys Leu Phe Ile
 100 105 110
 Asn Thr Thr Cys Ile Gly Lys Ile Ile Lys Pro Gly Ile Ser Ser Tyr
 115 120 125
 His Leu Gln Gln Gly Gln Ala Ile Ile Leu Ser Asp Thr Ile Ala Asn
 130 135 140
 His Gly Ala Ser Leu Phe Ala Met Arg Asn Glu Ile Lys Leu Lys Thr
 145 150 155 160
 Asn Leu Glu Ser Asp Cys Gln Leu Leu Tyr Pro Leu Leu Lys Pro Leu
 165 170 175
 Phe Leu Ser Asp Leu Lys Ile Asp Ala Leu Arg Asp Ala Thr Arg Gly
 180 185 190
 Gly Leu Ala Ser Val Leu Asn Glu Trp Ala Asn Ser Ser Arg Val Lys
 195 200 205
 Ile Val Ile Glu Glu Glu Lys Ile Pro Leu Lys Glu Glu Thr Lys Gly
 210 215 220
 Ile Cys Glu Ile Leu Gly Leu Glu Pro Tyr Ala Leu Ala Asn Glu Gly
 225 230 235 240
 Val Phe Val Leu Ala Leu Asn Gln Lys Asp Ala Pro Lys Ala Leu Glu
 245 250 255
 Ile Leu Lys Ser Asn Glu Lys Ala Lys Asn Ala Cys Val Ile Gly Lys
 260 265 270
 Val Phe Glu Asn Pro Tyr Pro Ser Val Val Leu Lys Asn Ala Trp Gly
 275 280 285
 Phe Glu Arg Ile Leu Glu Val Pro Glu Gly Glu Leu Leu Pro Arg Ile
 290 295 300

Cys

305

<210> 69

<211> 1977

<212> DNA

<213> Helicobacter pylori

<220>

<221> CDS

<222> (1)..(1977)

<400> 69

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Leu Asn Leu Leu Ser Gln Ile Pro Lys Asp Leu Gly Val Cys Lys Asp	
1 5 10 15	
ttg ttg aga gaa atc agg gat aaa aac tcc ccc tat ttt cat tac gct	96
Cys Leu Arg Glu Ile Arg Asp Lys Asn Ser Pro Tyr Phe His Tyr Ala	
20 25 30	
ttc aat tct tgc gcg aag tgt ggg gcg aga tac agc ctt tta aac gct	144
Phe Asn Ser Cys Ala Lys Cys Gly Ala Arg Tyr Ser Leu Leu Asn Ala	
35 40 45	
ttg ccc tat gac aga gaa aac tcc gcc cta aaa ccc ttc aaa ctc tgc	192
Leu Pro Tyr Asp Arg Glu Asn Ser Ala Leu Lys Pro Phe Lys Leu Cys	
50 55 60	
gat ttt tgt gct tct atc tat caa gac ccc acc aat aag cgc ttc cac	240
Asp Phe Cys Ala Ser Ile Tyr Gln Asp Pro Thr Asn Lys Arg Phe His	
65 70 75 80	
att caa ggc atc agc tgc aaa aag tgc ggt atc gcg ctc aat tac aag	288
Ile Gln Gly Ile Ser Cys Lys Lys Cys Gly Ile Ala Leu Asn Tyr Lys	
85 90 95	
cga ttc aaa aac gat gac gct ctt tta gaa tgc gct aaa gac att caa	336
Arg Phe Lys Asn Asp Asp Ala Leu Leu Glu Cys Ala Lys Asp Ile Gln	
100 105 110	
aag ggt aaa atc atc gct ctt aaa ggt ttg gga ggc ttt gct ctc ttg	384
Lys Gly Lys Ile Ile Ala Leu Lys Gly Leu Gly Gly Phe Ala Leu Leu	
115 120 125	
tgc gat gga agg aat ttt caa acc ata gaa aga tta cgg ctt tta aaa	432
Cys Asp Gly Arg Asn Phe Gln Thr Ile Glu Arg Leu Arg Leu Leu Lys	
130 135 140	
aac cgc ccc cta aag cct ttc gca ctc atg ttt aaa gat ttg aac aca	480
Asn Arg Pro Leu Lys Pro Phe Ala Leu Met Phe Lys Asp Leu Asn Thr	
145 150 155 160	
gcc aaa cag cat gcg ttt ttg aac gcg tta gaa tgc gag agc tta att	528
Ala Lys Gln His Ala Phe Leu Asn Ala Leu Glu Cys Glu Ser Leu Ile	
165 170 175	
tct aca agc gcc ccc att ctt tta gcg cgt aaa aaa cct gat ata aaa	576
Ser Thr Ser Ala Pro Ile Leu Leu Ala Arg Lys Lys Pro Asp Ile Lys	
180 185 190	
tta gcc ccc aat atc gct aaa aac tcc ccc ttt tat ggc gtg att ttg	624
Leu Ala Pro Asn Ile Ala Lys Asn Ser Pro Phe Tyr Gly Val Ile Leu	
195 200 205	
ccc tat acc cct ttg cat gct tta ttg ctg gat tta ttg gat ttc cct	672
Pro Tyr Thr Pro Leu His Ala Leu Leu Leu Asp Leu Leu Asp Phe Pro	
210 215 220	
att gtg ttc acg agc gcg aat ttc agc tcc ctc cct tta gcg agc gat	720
Ile Val Phe Thr Ser Ala Asn Phe Ser Ser Leu Pro Leu Ala Ser Asp	
225 230 235 240	
gag gct gag att gac gcc ttg agt ttc att ttt gat ttt aag ctc acg	768
Glu Ala Glu Ile Asp Ala Leu Ser Phe Ile Phe Asp Phe Lys Leu Thr	
245 250 255	
cac aac cgc gct atc atc cat agg att gat gac agc atc gtg cag cat	816
His Asn Arg Ala Ile Ile His Arg Ile Asp Asp Ser Ile Val Gln His	
260 265 270	
gtg gat aat gcc att cgc ccc atg cgt ttg gct agg ggg ttt gcc ccc	864
Val Asp Asn Ala Ile Arg Pro Met Arg Leu Ala Arg Gly Phe Ala Pro	
275 280 285	
ctt tac ctc acc ttg cct aaa cgc tct aat ggt tgc cca aaa aag att	912
Leu Tyr Leu Thr Leu Pro Lys Arg Ser Asn Gly Ser Pro Lys Lys Ile	
290 295 300	
tta gcg ctt gga gcg caa caa aaa ggg cat ttt agc tta ttg gat agc	960

Leu	Ala	Leu	Gly	Ala	Gln	Gln	Lys	Gly	His	Phe	Ser	Leu	Leu	Asp	Ser	
305					310					315					320	
gga	act	tcc	att	ctt	tta	ctc	tcg	cct	ttt	tgt	ggg	gat	ttg	agc	gtt	1008
Gly	Thr	Ser	Ile	Leu	Leu	Leu	Ser	Pro	Phe	Cys	Gly	Asp	Leu	Ser	Val	
				325					330					335		
tta	gaa	aat	gaa	aaa	cac	ttt	aaa	gaa	act	ttg	aat	ttt	ttc	tta	aaa	1056
Leu	Glu	Asn	Glu	Lys	His	Phe	Lys	Glu	Thr	Leu	Asn	Phe	Phe	Leu	Lys	
			340					345					350			
acc	tat	gat	ttt	aaa	ccc	acc	atc	tta	gct	tgc	gac	aag	cat	caa	aac	1104
Thr	Tyr	Asp	Phe	Lys	Pro	Thr	Ile	Leu	Ala	Cys	Asp	Lys	His	Gln	Asn	
		355					360					365				
tac	acc	acc	act	caa	atg	gct	ttt	gat	ttt	aat	acg	ccc	ttg	ttg	caa	1152
Tyr	Thr	Thr	Thr	Gln	Met	Ala	Phe	Asp	Phe	Asn	Thr	Pro	Leu	Leu	Gln	
		370				375				380						
gtc	cag	cac	cac	cat	gcc	cac	ttt	tta	gcg	agc	gtc	tta	gac	gca	ttg	1200
Val	Gln	His	His	His	Ala	His	Phe	Leu	Ala	Ser	Val	Leu	Asp	Ala	Leu	
385					390					395				400		
tta	caa	gat	ccg	cat	tta	aat	cac	ccc	ttt	ata	ggc	att	gtc	tgg	gat	1248
Leu	Gln	Asp	Pro	His	Leu	Asn	His	Pro	Phe	Ile	Gly	Ile	Val	Trp	Asp	
				405				410					415			
ggg	agt	ggg	gct	tat	gaa	aat	aag	att	tat	ggg	gcg	gag	tgt	ttt	gtg	1296
Gly	Ser	Gly	Ala	Tyr	Glu	Asn	Lys	Ile	Tyr	Gly	Ala	Glu	Cys	Phe	Val	
			420					425					430			
ggg	gat	ttg	gaa	cgc	att	gaa	gaa	acc	gcc	agg	ttt	gaa	gaa	ttt	tgg	1344
Gly	Asp	Leu	Glu	Arg	Ile	Glu	Glu	Thr	Ala	Arg	Phe	Glu	Glu	Phe	Trp	
		435				440					445					
ctt	tta	ggg	ggg	caa	aaa	gcg	atc	aaa	gag	cct	aga	cgc	ctg	gtt	tta	1392
Leu	Leu	Gly	Gly	Gln	Lys	Ala	Ile	Lys	Glu	Pro	Arg	Arg	Leu	Val	Leu	
		450				455				460						
gaa	atc	gct	tta	aaa	cac	caa	ctc	aac	aag	ctt	tta	aag	cgc	gtt	caa	1440
Glu	Ile	Ala	Leu	Lys	His	Gln	Leu	Asn	Lys	Leu	Leu	Lys	Arg	Val	Gln	
465				470					475					480		
aag	cat	ttt	aaa	gaa	gac	gaa	tta	gaa	att	ttc	caa	caa	atg	cat	gac	1488
Lys	His	Phe	Lys	Glu	Asp	Glu	Leu	Glu	Ile	Phe	Gln	Gln	Met	His	Asp	
			485					490					495			
aaa	aaa	att	caa	agc	ata	gcc	acc	aat	tcc	ata	ggg	cgt	ttg	ttt	gat	1536
Lys	Lys	Ile	Gln	Ser	Ile	Ala	Thr	Asn	Ser	Ile	Gly	Arg	Leu	Phe	Asp	
		500						505					510			
ata	gta	gcg	ttt	agt	ttg	gat	tta	aca	gga	acg	att	agc	ttt	gaa	gca	1584
Ile	Val	Ala	Phe	Ser	Leu	Asp	Leu	Thr	Gly	Thr	Ile	Ser	Phe	Glu	Ala	
		515				520						525				
gag	agc	ggg	cag	gtt	tta	gaa	aat	cta	gcc	tta	caa	agc	gat	gag	atc	1632
Glu	Ser	Gly	Gln	Val	Leu	Glu	Asn	Leu	Ala	Leu	Gln	Ser	Asp	Glu	Ile	
		530				535				540						
gct	ttt	tac	cct	ttt	gaa	atc	aaa	aac	agc	gtg	gtg	tgt	ttg	aaa	gaa	1680
Ala	Phe	Tyr	Pro	Phe	Glu	Ile	Lys	Asn	Ser	Val	Val	Cys	Leu	Lys	Glu	
545				550					555					560		
ttt	tat	caa	gcg	ttt	gaa	aag	gat	ttg	ggc	gtt	tta	gag	cct	gaa	cgc	1728
Phe	Tyr	Gln	Ala	Phe	Glu	Lys	Asp	Leu	Gly	Val	Leu	Glu	Pro	Glu	Arg	
			565					570					575			
atc	gct	aag	aaa	ttt	ttt	aac	agc	cta	gta	gaa	atc	att	acc	gct	tta	1776
Ile	Ala	Lys	Lys	Phe	Phe	Asn	Ser	Leu	Val	Glu	Ile	Ile	Thr	Ala	Leu	
			580					585					590			
atc	gtg	cct	ttt	aaa	gag	cat	gtg	gtg	gtg	tgc	agt	ggg	ggc	gtg	ttt	1824
Ile	Val	Pro	Phe	Lys	Glu	His	Val	Val	Val	Cys	Ser	Gly	Gly	Val	Phe	
		595				600						605				
tgc	aac	caa	tta	tta	tgc	gaa	caa	tta	gcc	aaa	cga	ttg	aga	ggg	cta	1872
Cys	Asn	Gln	Leu	Leu	Cys	Glu	Gln	Leu	Ala	Lys	Arg	Leu	Arg	Gly	Leu	
		610				615				620						
aag	agg	cag	tat	ttt	ttc	cac	aag	cat	ttc	ccc	cct	aat	gac	agc	agt	1920
Lys	Arg	Gln	Tyr	Phe	Phe	His	Lys	His	Phe	Pro	Pro	Asn	Asp	Ser	Ser	

[illegible]

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<211> 234

<212> DNA

<213> Helicobacter pylori

<220>

<221> CDS

<222> (1) .. (234)

<400> 71

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1 5 10 15

gtt aga aaa ttc tat cgg cat aaa aaa tgg gtg gat gca gat gtg tgg 96
Val Arg Lys Phe Tyr Arg His Lys Lys Trp Val Asp Ala Asp Val Trp
20 25 30

caa atg gaa aaa tta ctg cct gga aat gaa gtc ata gga cct gcg atc 144
Gln Met Glu Lys Leu Leu Pro Gly Asn Glu Val Ile Gly Pro Ala Ile

35 40 45
 gtg gaa tca gat gcg acc act ttc gtg ata ccc aaa ggc ttt gcg aca 192
 Val Glu Ser Asp Ala Thr Thr Phe Val Ile Pro Lys Gly Phe Ala Thr
 50 55 60

aga cta gac aaa cac cga ttg ttc cac ttg aaa gaa att aaa 234
Arg Leu Asp Lys His Arg Leu Phe His Leu Lys Glu Ile Lys
65 70 75

<210> 72

<211> 78

<212> PRT

<213> *Helicobacter pylori*

<400> 72

Val Glu Lys Glu His Gly Ala Thr Pro Pro Lys Glu Ala Lys Ile Gly
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 20 25 30
 Gln Met Glu Lys Leu Leu Pro Gly Asn Glu Val Ile Gly Pro Ala Ile
 35 40 45
 Val Glu Ser Asp Ala Thr Thr Phe Val Ile Pro Lys Gly Phe Ala Thr
 50 55 60
 Arg Leu Asp Lys His Arg Leu Phe His Leu Lys Glu Ile Lys
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<210> 73

<211> 383

<212> DNA

<213> Helicobacter pylori

<220>

<221> CDS

<222> (1)..(381)

<400> 73

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 1 5 10 15
 ttg ttt aaa ttc aac cgc ttg cac acc aaa atc tct att tta caa gat 96
 Leu Phe Lys Phe Asn Arg Leu His Thr Lys Ile Ser Ile Leu Gln Asp
 20 25 30
 gag aaa ccc atc tat tat gac aac acg att tta gat ccc aaa acc acc 144
 Glu Lys Pro Ile Tyr Tyr Asp Asn Thr Ile Leu Asp Pro Lys Thr Thr
 35 40 45
 gac tta aat aac atg tgc atg ttt gat ggc tat acg cat tat ttg aat 192
 Asp Leu Asn Asn Met Cys Met Phe Asp Gly Tyr Thr His Tyr Leu Asn
 50 55 60
 ttg gtg ctt gtc aat tgc ccc ata gag ctc tct ggt gtg cga gaa tgc 240
 Leu Val Leu Val Asn Cys Pro Ile Glu Leu Ser Gly Val Arg Glu Cys
 65 70 75 80
 att gaa gaa agc gaa ggg gtg gat ggg gca gtg agt gaa acc gct agt 288
 Ile Glu Glu Ser Glu Gly Val Asp Gly Ala Val Ser Glu Thr Ala Ser
 85 90 95
 tct cat tta tgc gtg aaa gct tta gcg aaa ggc tca gaa ccc tta ttg 336
 Ser His Leu Cys Val Lys Ala Leu Ala Lys Gly Ser Glu Pro Leu Leu
 100 105 110
 cat tta aga gaa aaa atc gct cgc ttg gtt acg caa acc acc acg ca 383
 His Leu Arg Glu Lys Ile Ala Arg Leu Val Thr Gln Thr Thr Thr
 115 120 125

<210> 74

<211> 127

<212> PRT

<213> Helicobacter pylori

<400> 74

Leu Leu Tyr Ser Glu Ile Ile Val Ala Gly Arg Val Ala Arg Asn Glu
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 Leu Phe Lys Phe Asn Arg Leu His Thr Lys Ile Ser Ile Leu Gln Asp
 20 25 30
 Glu Lys Pro Ile Tyr Tyr Asp Asn Thr Ile Leu Asp Pro Lys Thr Thr
 35 40 45
 Asp Leu Asn Asn Met Cys Met Phe Asp Gly Tyr Thr His Tyr Leu Asn
 50 55 60
 Leu Val Leu Val Asn Cys Pro Ile Glu Leu Ser Gly Val Arg Glu Cys
 65 70 75 80
 Ile Glu Glu Ser Glu Gly Val Asp Gly Ala Val Ser Glu Thr Ala Ser
 85 90 95
 Ser His Leu Cys Val Lys Ala Leu Ala Lys Gly Ser Glu Pro Leu Leu

100 105 110
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 Lys Glu Leu Leu Asn Asn His Phe Lys Gln Arg Leu Ala Phe Arg Cys
 1 5 10 15
 aat ggt gag aac ttg agc gct atc aaa gat tta cct cta tta aca 96
 Asn Gly Glu Asn Leu Ser Ala Ile Lys Lys Asp Leu Pro Leu Leu Thr
 20 25 30
 aac gaa ctc aac gcg cta ttt gta gag ctt tct aaa gac agc cat act 144
 Asn Glu Leu Asn Ala Leu Phe Val Glu Leu Ser Lys Asp Ser His Thr
 35 40 45
 gaa ttc agg cct ttc agc tta 165
 Glu Phe Arg Pro Phe Ser Leu
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 Asn Glu Leu Asn Ala Leu Phe Val Glu Leu Ser Lys Asp Ser His Thr
 35 40 45
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 Thr Ser Leu Asn Lys Leu Ile Tyr Thr Gly Gln Ile Ile Pro Asp Arg
 1 5 10 15
 ggt tcg tgg ttg tat ttt gaa tac gat tct aaa gat gtt tta tac gct 96
 Gly Ser Trp Leu Tyr Phe Glu Tyr Asp Ser Lys Asp Val Leu Tyr Ala
 20 25 30
 cgt atc aat aaa cgc cgt aaa gtg cct gtt acc att tta ttc agg gcg 144
 Arg Ile Asn Lys Arg Arg Lys Val Pro Val Thr Ile Leu Phe Arg Ala
 35 40 45
 atg gat tat caa aaa caa gac atc atc aaa atg ttc tac ccg ctt gtt 192
 Met Asp Tyr Gln Lys Gln Asp Ile Ile Lys Met Phe Tyr Pro Leu Val
 50 55 60
 aaa gtg cgt tat gaa aac gat aaa tat ttg atc ccg ttt gct tca tta 240
 Lys Val Arg Tyr Glu Asn Asp Lys Tyr Leu Ile Pro Phe Ala Ser Leu
 65 70 75 80
 gac gcc aat caa aga atg gaa ttt gac ttg aaa gat cct caa ggc aag 288
 Asp Ala Asn Gln Arg Met Glu Phe Asp Leu Lys Asp Pro Gln Gly Lys

	85	90	95	
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Val Ile Leu Leu Ala Gly Lys Lys Leu Thr Ser Arg Lys Ile Lys Glu				
	100	105	110	
ctt aaa gaa aac cat tta gaa tgg gtg gaa tac cct atg gat att tta				384
Leu Lys Glu Asn His Leu Glu Trp Val Glu Tyr Pro Met Asp Ile Leu				
	115	120	125	
ctc aat cgc cat tta gct gag cct gtt atg gta ggg aaa gaa gtc tta				432
Leu Asn Arg His Leu Ala Glu Pro Val Met Val Gly Lys Glu Val Leu				
	130	135	140	
ttg gac atg ctc act cag cta gat aaa aac aaa tta gaa aaa atc cac				480
Leu Asp Met Leu Thr Gln Leu Asp Lys Asn Lys Leu Glu Lys Ile His				
	145	150	155	
gat tta ggc gtg caa gaa ttt gtg atc atc aac gat ctg gcg tta ggg				528
Asp Leu Gly Val Gln Glu Phe Val Ile Ile Asn Asp Leu Ala Leu Gly				
	165	170	175	
cat gac gct tcc att atc caa tct ttt tca gcc gat tct gag tct ttg				576
His Asp Ala Ser Ile Ile Gln Ser Phe Ser Ala Asp Ser Glu Ser Leu				
	180	185	190	
aaa tta ctc aag caa acc gaa aaa att gat gat gaa aac gct cta gcg				624
Lys Leu Leu Lys Gln Thr Glu Lys Ile Asp Asp Glu Asn Ala Leu Ala				
	195	200	205	
gcg att cgt atc cat aag gtt atg aaa cca ggc gat ccc gtt acg act				672
Ala Ile Arg Ile His Lys Val Met Lys Pro Gly Asp Pro Val Thr Thr				
	210	215	220	
gaa gtg gct aag cag ttt gtc aaa aaa ctt ttc ttt gat cca gaa cgc				720
Glu Val Ala Lys Gln Phe Val Lys Lys Leu Phe Phe Asp Pro Glu Arg				
	225	230	235	
tat gat ttg acc atg gtg ggc cgc atg aaa atg aat cac aag tta ggc				768
Tyr Asp Leu Thr Met Val Gly Arg Met Lys Met Asn His Lys Leu Gly				
	245	250	255	
ttg cat gtg cct gat tac att acg act tta acg cat gaa gat att atc				816
Leu His Val Pro Asp Tyr Ile Thr Leu Thr His Glu Asp Ile Ile				
	260	265	270	
acc acc gtt aaa tac ctc atg aag atc aaa aac aat ca				854
Thr Thr Val Lys Tyr Leu Met Lys Ile Lys Asn Asn				
	275	280		
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Arg Ile Asn Lys Arg Arg Lys Val Pro Val Thr Ile Leu Phe Arg Ala				
35 40 45				
Met Asp Tyr Gln Lys Gln Asp Ile Ile Lys Met Phe Tyr Pro Leu Val				
50 55 60				
Lys Val Arg Tyr Glu Asn Asp Lys Tyr Leu Ile Pro Phe Ala Ser Leu				
65 70 75 80				
Asp Ala Asn Gln Arg Met Glu Phe Asp Leu Lys Asp Pro Gln Gly Lys				
85 90 95				
Val Ile Leu Leu Ala Gly Lys Lys Leu Thr Ser Arg Lys Ile Lys Glu				
100 105 110				
Leu Lys Glu Asn His Leu Glu Trp Val Glu Tyr Pro Met Asp Ile Leu				
115 120 125				
Leu Asn Arg His Leu Ala Glu Pro Val Met Val Gly Lys Glu Val Leu				
130 135 140				
Leu Asp Met Leu Thr Gln Leu Asp Lys Asn Lys Leu Glu Lys Ile His				

145 150 155 160
 Asp Leu Gly Val Gln Glu Phe Val Ile Ile Asn Asp Leu Ala Leu Gly
 165 170 175
 His Asp Ala Ser Ile Ile Gln Ser Phe Ser Ala Asp Ser Glu Ser Leu
 180 185 190
 Lys Leu Leu Lys Gln Thr Glu Lys Ile Asp Asp Glu Asn Ala Leu Ala
 195 200 205
 Ala Ile Arg Ile His Lys Val Met Lys Pro Gly Asp Pro Val Thr Thr
 210 215 220
 Glu Val Ala Lys Gln Phe Val Lys Lys Leu Phe Phe Asp Pro Glu Arg
 225 230 235 240
 Tyr Asp Leu Thr Met Val Gly Arg Met Lys Met Asn His Lys Leu Gly
 245 250 255
 Leu His Val Pro Asp Tyr Ile Thr Thr Leu Thr His Glu Asp Ile Ile
 260 265 270
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<210> 79

<211> 1843

<212> DNA

<213> Helicobacter pylori

<220>

<221> CDS

<222> (1)..(1842)

<400> 79

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 Arg Asp Ser Trp Gly Ala Ile Lys Ala Asn Arg Ala Gly Val Val Glu
 20 25 30
 aaa att gat tct aaa aat att tat att tta ggc gaa agc aaa gaa gaa 144
 Lys Ile Asp Ser Lys Asn Ile Tyr Ile Leu Gly Glu Ser Lys Glu Glu
 35 40 45
 gcc tat att gat gcg tat tct ttg caa aaa aac ttg cgc acc aac caa 192
 Ala Tyr Ile Asp Ala Tyr Ser Leu Gln Lys Asn Leu Arg Thr Asn Gln
 50 55 60
 aac acc agt ttc aat caa gtc cct atc gtt aaa gtg ggc gat aaa gtg 240
 Asn Thr Ser Phe Asn Gln Val Pro Ile Val Lys Val Gly Asp Lys Val
 65 70 75 80
 gga gcc ggg caa atc atc gct gat ggc cct agc atg gat aga ggc gag 288
 Gly Ala Gly Gln Ile Ile Ala Asp Gly Pro Ser Met Asp Arg Gly Glu
 85 90 95
 ttg gcg tta ggg aaa aat gtg cgc gtg gcg ttc atg cct tgg aat ggc 336
 Leu Ala Leu Gly Lys Asn Val Arg Val Ala Phe Met Pro Trp Asn Gly
 100 105 110
 tat aac ttt gaa gac gcg atc gtg gtg agt gag tgc atc act aaa gat 384
 Tyr Asn Phe Glu Asp Ala Ile Val Val Ser Glu Cys Ile Thr Lys Asp
 115 120 125
 gat att ttc act tcc acc cac att tat gaa aaa gaa gtg gat gct agg 432
 Asp Ile Phe Thr Ser Thr His Ile Tyr Glu Lys Glu Val Asp Ala Arg
 130 135 140
 gag ctt aag cat ggt gtg gaa gaa ttt acc gct gat att cct gat gtg 480
 Glu Leu Lys His Gly Val Glu Glu Phe Thr Ala Asp Ile Pro Asp Val
 145 150 155 160
 aaa gaa gaa gcg ctc gct cat ctt gat gaa agc ggg atc gtt aaa gtc 528
 Lys Glu Glu Ala Leu Ala His Leu Asp Glu Ser Gly Ile Val Lys Val
 165 170 175
 ggt act tat gtg agc gct ggc atg att ttg gtg ggc aaa act tct cct 576
 Gly Thr Tyr Val Ser Ala Gly Met Ile Leu Val Gly Lys Thr Ser Pro
 180 185 190

aaa ggc gag att aaa agc acg cct gaa gag cgg ctt tta agg gct att	624
Lys Gly Glu Ile Lys Ser Thr Pro Glu Glu Arg Leu Leu Arg Ala Ile	
195 200 205	
ttt ggg gat aaa gcc ggg cat gtg gtc aat aag agt ttg tat tgc cct	672
Phe Gly Asp Lys Ala Gly His Val Val Asn Lys Ser Leu Tyr Cys Pro	
210 215 220	
ccc agt ttg gaa ggc acg gtg att gat gtg aaa gtc ttc act aaa aaa	720
Pro Ser Leu Glu Gly Thr Val Ile Asp Val Lys Val Phe Thr Lys Lys	
225 230 235 240	
ggc tat gag aaa gac gcg cga gtt ttg agc gcg tat gaa gaa gaa aaa	768
Gly Tyr Glu Lys Asp Ala Arg Val Leu Ser Ala Tyr Glu Glu Glu Lys	
245 250 255	
gcc aag ctt gat atg gag cat ttt gat cgc ttg acc atg ctc aat aga	816
Ala Lys Leu Asp Met Glu His Phe Asp Arg Leu Thr Met Leu Asn Arg	
260 265 270	
gaa gaa ttg ttg cgc gtt agc tcg ctc ctt tct caa gcg att tta gaa	864
Glu Glu Leu Leu Arg Val Ser Ser Leu Ser Gln Ala Ile Leu Glu	
275 280 285	
gag cct ttc agc cat aac ggc aag gat tat aaa gaa ggc gat caa atc	912
Glu Pro Phe Ser His Asn Gly Lys Asp Tyr Lys Glu Gly Asp Gln Ile	
290 295 300	
cct aaa gaa gaa atc gct tca atc aac cgc ttc act ttg gct agt ttg	960
Pro Lys Glu Glu Ile Ala Ser Ile Asn Arg Phe Thr Leu Ala Ser Leu	
305 310 315 320	
gtc aaa aag tat tct aaa gaa gtg caa aac cac tat gaa atc act aaa	1008
Val Lys Lys Tyr Ser Lys Glu Val Gln Asn His Tyr Glu Ile Thr Lys	
325 330 335	
aac aat ttc tta gag caa aag aaa gtt ttg ggc gaa gag cat gaa gaa	1056
Asn Asn Phe Leu Glu Gln Lys Lys Val Leu Gly Glu Glu His Glu Glu	
340 345 350	
aag ctt tct att tta gaa aaa gat gat att ttg cct aat ggc gtg atc	1104
Lys Leu Ser Ile Leu Glu Lys Asp Asp Ile Leu Pro Asn Gly Val Ile	
355 360 365	
aaa aaa gtc aag ctc tat atc gct aca aaa cga aag ctt aaa gtg ggc	1152
Lys Lys Val Lys Leu Tyr Ile Ala Thr Lys Arg Lys Leu Lys Val Gly	
370 375 380	
gat aaa atg gca gga agg cat ggg aat aaa ggg att gtg tct aat atc	1200
Asp Lys Met Ala Gly Arg His Gly Asn Lys Gly Ile Val Ser Asn Ile	
385 390 395 400	
gtg ccg gtt gcg gat atg cct tat acc gct gat ggc gag cct gta gat	1248
Val Pro Val Ala Asp Met Pro Tyr Thr Ala Asp Gly Glu Pro Val Asp	
405 410 415	
att gtt tta aac cct tta ggc gtg cca agc cgc atg aat atc ggg cag	1296
Ile Val Leu Asn Pro Leu Gly Val Pro Ser Arg Met Asn Ile Gly Gln	
420 425 430	
att tta gaa atg cat tta ggc tta gtg ggg aaa gaa ttt ggg aag caa	1344
Ile Leu Glu Met His Leu Gly Leu Val Gly Lys Glu Phe Gly Lys Gln	
435 440 445	
atc gct cgc atg cta gag gat aaa acc aaa gat ttt gcc aaa gaa ttg	1392
Ile Ala Arg Met Leu Glu Asp Lys Thr Lys Asp Phe Ala Lys Glu Leu	
450 455 460	
cgt gct aaa atg cta gaa atc gct aac gct att aat gaa aaa gac ccc	1440
Arg Ala Lys Met Leu Glu Ile Ala Asn Ala Ile Asn Glu Lys Asp Pro	
465 470 475 480	
ttg aca atc cat gcg ctt gag aat tgt tct gat gaa gag ctt ttg gaa	1488
Leu Thr Ile His Ala Leu Glu Asn Cys Ser Asp Glu Glu Leu Leu Glu	
485 490 495	
tac gca aaa gat tgg agc aag ggc gtt aag atg gct atc cct gtg ttt	1536
Tyr Ala Lys Asp Trp Ser Lys Gly Val Lys Met Ala Ile Pro Val Phe	
500 505 510	
gaa ggc atc tcg caa gaa aaa ttt tat aag cta ttt gaa tta gct aag	1584

Glu Gly Ile Ser Gln Glu Lys Phe Tyr Lys Leu Phe Glu Leu Ala Lys
 515 520 525
 atc gct atg gat ggc aaa atg gat ctg tat gac gga cgc aca ggc gag 1632
 Ile Ala Met Asp Gly Lys Met Asp Leu Tyr Asp Gly Arg Thr Gly Glu
 530 535 540
 aaa atg agg gag cgc gtg aat gtg ggc tac atg tat atg atc aaa ctc 1680
 Lys Met Arg Glu Arg Val Asn Val Gly Tyr Met Tyr Met Ile Lys Leu
 545 550 555 560
 cac cat tta gtg gat gaa aaa gtc cat gcc aga agc aca ggc cct tat 1728
 His His Leu Val Asp Glu Lys Val His Ala Arg Ser Thr Gly Pro Tyr
 565 570 575
 agc tta gta acg cac cag ccc gtg ggg ggt aaa gcg ctc ttt ggg ggt 1776
 Ser Leu Val Thr His Gln Pro Val Gly Gly Lys Ala Leu Phe Gly Gly
 580 585 590
 caa agg ttt ggg gaa atg gaa gtg tgg gcc ttg gaa gct tat ggc gca 1824
 Gln Arg Phe Gly Glu Met Glu Val Trp Ala Leu Glu Ala Tyr Gly Ala
 595 600 605
 gcg cac act cta aaa gaa a 1843
 Ala His Thr Leu Lys Glu
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 <213> Helicobacter pylori
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 20 25 30
 Lys Ile Asp Ser Lys Asn Ile Tyr Ile Leu Gly Glu Ser Lys Glu Glu
 35 40 45
 Ala Tyr Ile Asp Ala Tyr Ser Leu Gln Lys Asn Leu Arg Thr Asn Gln
 50 55 60
 Asn Thr Ser Phe Asn Gln Val Pro Ile Val Lys Val Gly Asp Lys Val
 65 70 75 80
 Gly Ala Gly Gln Ile Ile Ala Asp Gly Pro Ser Met Asp Arg Gly Glu
 85 90 95
 Leu Ala Leu Gly Lys Asn Val Arg Val Ala Phe Met Pro Trp Asn Gly
 100 105 110
 Tyr Asn Phe Glu Asp Ala Ile Val Val Ser Glu Cys Ile Thr Lys Asp
 115 120 125
 Asp Ile Phe Thr Ser Thr His Ile Tyr Glu Lys Glu Val Asp Ala Arg
 130 135 140
 Glu Leu Lys His Gly Val Glu Glu Phe Thr Ala Asp Ile Pro Asp Val
 145 150 155 160
 Lys Glu Glu Ala Leu Ala His Leu Asp Glu Ser Gly Ile Val Lys Val
 165 170 175
 Gly Thr Tyr Val Ser Ala Gly Met Ile Leu Val Gly Lys Thr Ser Pro
 180 185 190
 Lys Gly Glu Ile Lys Ser Thr Pro Glu Glu Arg Leu Leu Arg Ala Ile
 195 200 205
 Phe Gly Asp Lys Ala Gly His Val Val Asn Lys Ser Leu Tyr Cys Pro
 210 215 220
 Pro Ser Leu Glu Gly Thr Val Ile Asp Val Lys Val Phe Thr Lys Lys
 225 230 235 240
 Gly Tyr Glu Lys Asp Ala Arg Val Leu Ser Ala Tyr Glu Glu Glu Lys
 245 250 255
 Ala Lys Leu Asp Met Glu His Phe Asp Arg Leu Thr Met Leu Asn Arg
 260 265 270
 Glu Glu Leu Leu Arg Val Ser Ser Leu Leu Ser Gln Ala Ile Leu Glu
 275 280 285

Glu Pro Phe Ser His Asn Gly Lys Asp Tyr Lys Glu Gly Asp Gln Ile
 290 295 300
 Pro Lys Glu Glu Ile Ala Ser Ile Asn Arg Phe Thr Leu Ala Ser Leu
 305 310 315 320
 Val Lys Lys Tyr Ser Lys Glu Val Gln Asn His Tyr Glu Ile Thr Lys
 325 330 335
 Asn Asn Phe Leu Glu Gln Lys Lys Val Leu Gly Glu Glu His Glu Glu
 340 345 350
 Lys Leu Ser Ile Leu Glu Lys Asp Asp Ile Leu Pro Asn Gly Val Ile
 355 360 365
 Lys Lys Val Lys Leu Tyr Ile Ala Thr Lys Arg Lys Leu Lys Val Gly
 370 375 380
 Asp Lys Met Ala Gly Arg His Gly Asn Lys Gly Ile Val Ser Asn Ile
 385 390 395 400
 Val Pro Val Ala Asp Met Pro Tyr Thr Ala Asp Gly Glu Pro Val Asp
 405 410 415
 Ile Val Leu Asn Pro Leu Gly Val Pro Ser Arg Met Asn Ile Gly Gln
 420 425 430
 Ile Leu Glu Met His Leu Gly Leu Val Gly Lys Glu Phe Gly Lys Gln
 435 440 445
 Ile Ala Arg Met Leu Glu Asp Lys Thr Lys Asp Phe Ala Lys Glu Leu
 450 455 460
 Arg Ala Lys Met Leu Glu Ile Ala Asn Ala Ile Asn Glu Lys Asp Pro
 465 470 475 480
 Leu Thr Ile His Ala Leu Glu Asn Cys Ser Asp Glu Glu Leu Leu Glu
 485 490 495
 Tyr Ala Lys Asp Trp Ser Lys Gly Val Lys Met Ala Ile Pro Val Phe
 500 505 510
 Glu Gly Ile Ser Gln Glu Lys Phe Tyr Lys Leu Phe Glu Leu Ala Lys
 515 520 525
 Ile Ala Met Asp Gly Lys Met Asp Leu Tyr Asp Gly Arg Thr Gly Glu
 530 535 540
 Lys Met Arg Glu Arg Val Asn Val Gly Tyr Met Tyr Met Ile Lys Leu
 545 550 555 560
 His His Leu Val Asp Glu Lys Val His Ala Arg Ser Thr Gly Pro Tyr
 565 570 575
 Ser Leu Val Thr His Gln Pro Val Gly Gly Lys Ala Leu Phe Gly Gly
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 Gln Arg Phe Gly Glu Met Glu Val Trp Ala Leu Glu Ala Tyr Gly Ala
 595 600 605
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<211> 1040

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<213> Helicobacter pylori

<220>

<221> CDS

<222> (1)..(1038)

<400> 81

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 tta gat aaa gtt gtt gct aaa aaa gag cca gag agt ttt ctc aag ccg 96
 Leu Asp Lys Val Val Ala Lys Lys Glu Pro Glu Ser Phe Leu Lys Pro
 20 25 30
 atc atc tca cca ata gag gac tac caa aag agt gtc agg caa att caa 144
 Ile Ile Ser Pro Ile Glu Asp Tyr Gln Lys Ser Val Arg Gln Ile Gln
 35 40 45
 gcg caa ttc aca gac gcg cca aag ttc aat gaa gag ggc gct tac cca 192
 Ala Gln Phe Thr Asp Ala Pro Lys Phe Asn Glu Glu Gly Ala Tyr Pro

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65	70	75	80
agc atg gaa ttt tgc ttg cct aaa gtt tat cct ttc ccc cct aaa agc			288
Ser Met Glu Phe Cys Leu Pro Lys Val Tyr Pro Phe Pro Pro Lys Ser			
85	90	95	
ttg tat ata gag cat gaa aaa gac ggg cag ttt tta aga gaa atg ctc			336
Leu Tyr Ile Glu His Glu Lys Asp Gly Gln Phe Leu Arg Glu Met Leu			
100	105	110	
atg cgc ttg cta tcc agt gcg cct tta gtg caa tta gaa gtg atc tta			384
Met Arg Leu Leu Ser Ser Ala Pro Leu Val Gln Leu Glu Val Ile Leu			
115	120	125	
gtt gat gcg ctg agc cta ggg ggc att ttc aat ctg gca aga agg ctt			432
Val Asp Ala Leu Ser Leu Gly Gly Ile Phe Asn Leu Ala Arg Arg Leu			
130	135	140	
tta cat aaa gac aat gac ttt att tac cag caa agg att tta act gaa			480
Leu His Lys Asp Asn Asp Phe Ile Tyr Gln Gln Arg Ile Leu Thr Glu			
145	150	155	160
agc aag gaa ata gaa gaa gcc cta aag cat ttg tat gaa tat tta aag			528
Ser Lys Glu Ile Glu Glu Ala Leu Lys His Leu Tyr Glu Tyr Leu Lys			
165	170	175	
gtt aat ttg caa gaa aaa tta gcc ggt tat aaa gat ttt gcg cat tat			576
Val Asn Leu Gln Glu Lys Leu Ala Gly Tyr Lys Asp Phe Ala His Tyr			
180	185	190	
aat gaa gaa aaa aaa gac cgc ttg cct tta aaa gcg ctt ttt tta agc			624
Asn Glu Glu Lys Lys Asp Arg Leu Pro Leu Lys Ala Leu Phe Leu Ser			
195	200	205	
ggg gta gat gct tta agt caa aac gcg ctt tat tat ctg gaa aaa atc			672
Gly Val Asp Ala Leu Ser Gln Asn Ala Leu Tyr Tyr Leu Glu Lys Ile			
210	215	220	
atg cgt ttt ggc tct aaa aat ggg gtt ttg agc ttt gtc aat ttg gag			720
Met Arg Phe Gly Ser Lys Asn Gly Val Leu Ser Phe Val Asn Leu Glu			
225	230	235	240
agt gaa aaa aat aat aaa tcc aca gaa gat ttg aaa cgc tat gcg gag			768
Ser Glu Lys Asn Asn Lys Ser Thr Glu Asp Leu Lys Arg Tyr Ala Glu			
245	250	255	
tgt ttt aaa gac agg aca agt ttt gaa cgc tta aaa tat ctt aat ata			816
Cys Phe Lys Asp Arg Thr Ser Phe Glu Arg Leu Lys Tyr Leu Asn Ile			
260	265	270	
gaa gtg atc aat gat cat ggt atc caa tct aag cac atg aaa gac ttc			864
Glu Val Ile Asn Asp His Gly Ile Gln Ser Lys His Met Lys Asp Phe			
275	280	285	
gct gat aaa att aaa gcg tat tac gag aaa aag aaa gca gtt aaa agg			912
Ala Asp Lys Ile Lys Ala Tyr Tyr Glu Lys Lys Lys Ala Val Lys Arg			
290	295	300	
gag ttg aaa gac tta caa aaa gac gaa aaa ttt tgg act gaa agc tct			960
Glu Leu Lys Asp Leu Gln Lys Asp Glu Lys Phe Trp Thr Glu Ser Ser			
305	310	315	320
cag ttt aaa gtg tct gtg ccg gtg ggg tgg gat att aac cat aag gaa			1008
Gln Phe Lys Val Ser Val Pro Val Gly Trp Asp Ile Asn His Lys Glu			
325	330	335	
gtg tgt ttt gaa atc ggt aac gaa caa aac ca			1040
Val Cys Phe Glu Ile Gly Asn Glu Gln Asn			
340	345		

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 <212> PRT
 <213> Helicobacter pylori
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 35 40 45
 Ala Gln Phe Thr Asp Ala Pro Lys Phe Asn Glu Glu Gly Ala Tyr Pro
 50 55 60
 Gln Phe Leu Ser Cys Gly Leu Leu Glu Ile Lys Gly Lys Asn Gly Ala
 65 70 75 80
 Ser Met Glu Phe Cys Leu Pro Lys Val Tyr Pro Phe Pro Pro Lys Ser
 85 90 95
 Leu Tyr Ile Glu His Glu Lys Asp Gly Gln Phe Leu Arg Glu Met Leu
 100 105 110
 Met Arg Leu Leu Ser Ser Ala Pro Leu Val Gln Leu Glu Val Ile Leu
 115 120 125
 Val Asp Ala Leu Ser Leu Gly Gly Ile Phe Asn Leu Ala Arg Arg Leu
 130 135 140
 Leu His Lys Asp Asn Asp Phe Ile Tyr Gln Gln Arg Ile Leu Thr Glu
 145 150 155 160
 Ser Lys Glu Ile Glu Glu Ala Leu Lys His Leu Tyr Glu Tyr Leu Lys
 165 170 175
 Val Asn Leu Gln Glu Lys Leu Ala Gly Tyr Lys Asp Phe Ala His Tyr
 180 185 190
 Asn Glu Glu Lys Lys Asp Arg Leu Pro Leu Lys Ala Leu Phe Leu Ser
 195 200 205
 Gly Val Asp Ala Leu Ser Gln Asn Ala Leu Tyr Tyr Leu Glu Lys Ile
 210 215 220
 Met Arg Phe Gly Ser Lys Asn Gly Val Leu Ser Phe Val Asn Leu Glu
 225 230 235 240
 Ser Glu Lys Asn Asn Lys Ser Thr Glu Asp Leu Lys Arg Tyr Ala Glu
 245 250 255
 Cys Phe Lys Asp Arg Thr Ser Phe Glu Arg Leu Lys Tyr Leu Asn Ile
 260 265 270
 Glu Val Ile Asn Asp His Gly Ile Gln Ser Lys His Met Lys Asp Phe
 275 280 285
 Ala Asp Lys Ile Lys Ala Tyr Glu Lys Lys Lys Ala Val Lys Arg
 290 295 300
 Glu Leu Lys Asp Leu Gln Lys Asp Glu Lys Phe Trp Thr Glu Ser Ser
 305 310 315 320
 Gln Phe Lys Val Ser Val Pro Val Gly Trp Asp Ile Asn His Lys Glu
 325 330 335
 Val Cys Phe Glu Ile Gly Asn Glu Gln Asn
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<210> 83

<211> 63

<212> DNA

<213> Helicobacter pylori

<220>

<221> CDS

<222> (1)..(63)

<400> 83

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1 5 10 15
 att tct aaa ttc ttt

Ile Ser Lys Phe Phe
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<210> 84

<211> 21

<212> PRT

<213> Helicobacter pylori

63

<400> 84

Ile Lys Pro Thr Glu Gln Lys Gly Phe Phe Lys Ser Phe Leu Asp Lys
 1 5 10 15
 Ile Ser Lys Phe Phe
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<210> 85

<211> 846

<212> DNA

<213> *Helicobacter pylori*

<220>

<221> CDS

<222> (1)..(846)

<400> 85

gtg ttc aaa gac agc aaa aaa gac gct tgc ggg ttc atc tat gag atc 48
 Val Phe Lys Asp Ser Lys Lys Asp Ala Cys Gly Phe Ile Tyr Glu Ile
 1 5 10 15
 agc gag ttc atg aaa gcc tat acc gca ttg cta aaa aaa caa gac cga 96
 Ser Glu Phe Met Lys Ala Tyr Thr Ala Leu Leu Lys Lys Gln Asp Arg
 20 25 30
 tac gtc tat tta ttg agg tat ctc ccc tct agg tat tgg gcc agc att 144
 Tyr Val Tyr Leu Leu Arg Tyr Leu Pro Ser Arg Tyr Trp Ala Ser Ile
 35 40 45
 tta acg act gcc ctt tat gtc aaa tac cct gat ttt gac gct ttg aaa 192
 Leu Thr Thr Ala Leu Tyr Val Lys Tyr Pro Asp Phe Asp Ala Leu Lys
 50 55 60
 aag ctt ttg gtg tct tat tat tac caa act tgg att gca gga ggc acg 240
 Lys Leu Leu Val Ser Tyr Tyr Tyr Gln Thr Trp Ile Ala Gly Gly Thr
 65 70 75 80
 atc acg cgc atc aag caa acc agt atc aac att atc aaa aac gtt aaa 288
 Ile Thr Arg Ile Lys Gln Thr Ser Ile Asn Ile Ile Lys Asn Val Lys
 85 90 95
 agc aat aag agc gtt gaa acc atc aaa gag ctt ata ttg aat agc atc 336
 Ser Asn Lys Ser Val Glu Thr Ile Lys Glu Leu Ile Leu Asn Ser Ile
 100 105 110
 gac tct tat aac acc ttt gat caa tac ctc tat aac tta tgg gat agc 384
 Asp Ser Tyr Asn Thr Phe Asp Gln Tyr Leu Tyr Asn Leu Trp Asp Ser
 115 120 125
 tct tct gtt tat cat agc aaa tgg gtg cgt cct gtc tta gcc cta gct 432
 Ser Ser Val Tyr His Ser Lys Trp Val Arg Pro Val Leu Ala Leu Ala
 130 135 140
 aat tat ttc atg gca gat gaa gag aaa ccc cat ttt atc gct atg gat 480
 Asn Tyr Phe Met Ala Asp Glu Glu Lys Pro His Phe Ile Ala Met Asp
 145 150 155 160
 gcc gaa acc caa gtg gag cat att ttg cca caa acg ccc aaa aga ggc 528
 Ala Glu Thr Gln Val Glu His Ile Leu Pro Gln Thr Pro Lys Arg Gly
 165 170 175
 agt caa tgg aac gcg gat ttt gac aaa gaa aaa aga gaa gaa tgg gta 576
 Ser Gln Trp Asn Ala Asp Phe Asp Lys Glu Lys Arg Glu Glu Trp Val
 180 185 190
 aat aat atc gcg aat tta acc ctt tta aag cgt aaa aag aac gcg cat 624
 Asn Asn Ile Ala Asn Leu Thr Leu Leu Lys Arg Lys Lys Asn Ala His
 195 200 205
 gct tta aac ggg gat ttt gat gaa aaa aga aaa att tat gga ggc aaa 672
 Ala Leu Asn Gly Asp Phe Asp Glu Lys Arg Lys Ile Tyr Gly Gly Lys
 210 215 220
 gac acg agc aaa gtg att agc tgt tat gac atc act aaa gaa ttg tat 720
 Asp Thr Ser Lys Val Ile Ser Cys Tyr Asp Ile Thr Lys Glu Leu Tyr
 225 230 235 240
 agc aat tat agg aag tgg aat gag aag tcc ctc caa gag cga tac aaa 768
 Ser Asn Tyr Arg Lys Trp Asn Glu Lys Ser Leu Gln Glu Arg Tyr Lys
 245 250 255

846

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<211> 282

<212> PRT

<213> *Helicobacter pylori*

<400> 86

<400> 86															
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Ser	Glu	Phe	Met	Lys	Ala	Tyr	Thr	Ala	Leu	Leu	Lys	Lys	Gln	Asp	Arg
			20					25					30		
Tyr	Val	Tyr	Leu	Leu	Arg	Tyr	Leu	Pro	Ser	Arg	Tyr	Trp	Ala	Ser	Ile
		35					40					45			
Leu	Thr	Thr	Ala	Leu	Tyr	Val	Lys	Tyr	Pro	Asp	Phe	Asp	Ala	Leu	Lys
	50					55					60				
Lys	Leu	Leu	Val	Ser	Tyr	Tyr	Gln	Thr	Trp	Ile	Ala	Gly	Gly	Thr	
65					70				75					80	
Ile	Thr	Arg	Ile	Lys	Gln	Thr	Ser	Ile	Asn	Ile	Ile	Lys	Asn	Val	Lys
				85					90					95	
Ser	Asn	Lys	Ser	Val	Glu	Thr	Ile	Lys	Glu	Leu	Ile	Leu	Asn	Ser	Ile
			100					105					110		
Asp	Ser	Tyr	Asn	Thr	Phe	Asp	Gln	Tyr	Leu	Tyr	Asn	Leu	Trp	Asp	Ser
		115					120					125			
Ser	Ser	Val	Tyr	His	Ser	Lys	Trp	Val	Arg	Pro	Val	Leu	Ala	Leu	Ala
	130					135					140				
Asn	Tyr	Phe	Met	Ala	Asp	Glu	Glu	Lys	Pro	His	Phe	Ile	Ala	Met	Asp
145					150					155				160	
Ala	Glu	Thr	Gln	Val	Glu	His	Ile	Leu	Pro	Gln	Thr	Pro	Lys	Arg	Gly
			165						170					175	
Ser	Gln	Trp	Asn	Ala	Asp	Phe	Asp	Lys	Glu	Lys	Arg	Glu	Glu	Trp	Val
			180					185					190		
Asn	Asn	Ile	Ala	Asn	Leu	Thr	Leu	Leu	Lys	Arg	Lys	Lys	Asn	Ala	His
	195						200					205			
Ala	Leu	Asn	Gly	Asp	Phe	Asp	Glu	Lys	Arg	Lys	Ile	Tyr	Gly	Gly	Lys
	210					215					220				
Asp	Thr	Ser	Lys	Val	Ile	Ser	Cys	Tyr	Asp	Ile	Thr	Lys	Glu	Leu	Tyr
225					230					235				240	
Ser	Asn	Tyr	Arg	Lys	Trp	Asn	Glu	Lys	Ser	Leu	Gln	Glu	Arg	Tyr	Lys
			245						250					255	
Ser	Leu	Tyr	Asn	Thr	Ile	Thr	Pro	Val	Leu	His	Ile	Glu	Gly	Gln	Glu
			260					265					270		
Asp	Asp	Phe	Glu	Asp	Asp	Phe	Asp	Leu	Glu						
		275					280								

<210> 87

<211> 334

<212> DNA

<213> *Helicobacter pylori*

<220>

<221> CDS

<222> (1) .. (333)

<400> 87

<400> 87																
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Tyr	Gly	Glu	Phe	Leu	Glu	Lys	Glu	Lys	Glu	Gly	Phe	Met	Val	Asp	Glu	
1				5					10					15		
caa	aac	cct	tat	ccg	gaa	gaa	gtc	cgc	ttt	aat	gag	ttg	cgt	tta	gcg	96
Gln	Asn	Pro	Tyr	Pro	Glu	Glu	Val	Arg	Phe	Asn	Glu	Leu	Arg	Leu	Ala	
			20					25					30			

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gaa ttt gag agc gtt ttt agc gcc att gtg cct tta gag gat tta gat 144
Glu Phe Glu Ser Val Phe Ser Ala Ile Val Pro Leu Glu Asp Leu Asp
      35                40                45
aaa cct gca tgc gct cat cat gcc cta aag gct tta gaa gcc acg ctt 192
Lys Pro Ala Cys Ala His His Ala Leu Lys Ala Leu Glu Ala Thr Leu
      50                55                60
aaa aat agg gat ttg ggc ttt gat gcg aca gaa ttg gaa cag atc gca 240
Lys Asn Arg Asp Leu Gly Phe Asp Ala Thr Glu Leu Glu Gln Ile Ala
      65                70                75                80
aaa ggt ttc att cct aag ggg tat ttg tgg cat ttt gac gcg aat gtt 288
Lys Gly Phe Ile Pro Lys Gly Tyr Leu Trp His Phe Asp Ala Asn Val
      85                90                95
tta ggg aat gtg gcg ttg gtg aga gaa gag tta tta tta ggc gtg a 334
Leu Gly Asn Val Ala Leu Val Arg Glu Glu Leu Leu Leu Gly Val
      100                105                110

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<210> 88

<211> 111

<212> PRT

<213> Helicobacter pylori

<400> 88

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Tyr Gly Glu Phe Leu Glu Lys Glu Lys Glu Gly Phe Met Val Asp Glu
1      5      10
Gln Asn Pro Tyr Pro Glu Glu Val Arg Phe Asn Glu Leu Arg Leu Ala
      20      25      30
Glu Phe Glu Ser Val Phe Ser Ala Ile Val Pro Leu Glu Asp Leu Asp
      35      40      45
Lys Pro Ala Cys Ala His His Ala Leu Lys Ala Leu Glu Ala Thr Leu
      50      55      60
Lys Asn Arg Asp Leu Gly Phe Asp Ala Thr Glu Leu Glu Gln Ile Ala
      65      70      75      80
Lys Gly Phe Ile Pro Lys Gly Tyr Leu Trp His Phe Asp Ala Asn Val
      85      90      95
Leu Gly Asn Val Ala Leu Val Arg Glu Glu Leu Leu Leu Gly Val
      100      105      110

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<210> 89

<211> 1692

<212> DNA

<213> Helicobacter pylori

<220>

<221> CDS

<222> (1)..(1692)

<400> 89

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1      5      10      15
att aaa aaa acc gaa gaa aag caa aaa gtt tta gat gaa gaa tta gaa 96
Ile Lys Lys Thr Glu Glu Lys Gln Lys Val Leu Asp Glu Glu Leu Glu
      20      25      30
gat ggc tat gac ttt ttg aaa gaa aag gat ttt tta gag tgg agc aga 144
Asp Gly Tyr Asp Phe Leu Lys Glu Lys Asp Phe Leu Glu Trp Ser Arg
      35      40      45
agc gat agc cca gtg cgc atg tat ttg cgc gaa atg ggg gat ata aaa 192
Ser Asp Ser Pro Val Arg Met Tyr Leu Arg Glu Met Gly Asp Ile Lys
      50      55      60
ctt tta agc aaa gat gaa gag att gaa ttg agc aag caa atc cgc ttg 240
Leu Leu Ser Lys Asp Glu Glu Ile Glu Leu Ser Lys Gln Ile Arg Leu
      65      70      75      80
ggt gaa gac att att tta gac gcg atc tgc tgc gtg ccg tat ttg att 288
Gly Glu Asp Ile Ile Leu Asp Ala Ile Cys Ser Val Pro Tyr Leu Ile
      85      90      95
gat ttt atc tat gcg tat aaa gac gct tta atc aat cgt gaa aga agg 336

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Asp	Phe	Ile	Tyr	Ala	Tyr	Lys	Asp	Ala	Leu	Ile	Asn	Arg	Glu	Arg	Arg	
			100				105						110			
gtt	aaa	gag	ctt	ttc	agg	agc	ttt	gat	gat	gac	gat	gaa	aat	agc	gtg	384
Val	Lys	Glu	Leu	Phe	Arg	Ser	Phe	Asp	Asp	Asp	Asp	Glu	Asn	Ser	Val	
		115					120					125				
agc	gat	tct	aaa	aaa	gat	gaa	gac	aac	gaa	gaa	gat	gaa	gaa	aac	gaa	432
Ser	Asp	Ser	Lys	Lys	Asp	Glu	Asp	Asn	Glu	Glu	Asp	Glu	Glu	Asn	Glu	
		130					135				140					
gaa	agg	aaa	aaa	gtc	gtt	tct	gaa	aaa	gac	aag	aag	cgt	gta	gaa	aag	480
Glu	Arg	Lys	Lys	Val	Val	Ser	Glu	Lys	Asp	Lys	Lys	Arg	Val	Glu	Lys	
145					150					155					160	
gtt	caa	gaa	agc	ttt	aaa	gcc	cta	gac	aag	gct	aaa	aaa	gaa	tgg	ctt	528
Val	Gln	Glu	Ser	Phe	Lys	Ala	Leu	Asp	Lys	Ala	Lys	Lys	Glu	Trp	Leu	
				165					170					175		
aaa	gcc	ctt	gaa	gcc	ccc	ata	gat	gaa	aga	gaa	gac	gaa	ttg	gtg	cgt	576
Lys	Ala	Leu	Glu	Ala	Pro	Ile	Asp	Glu	Arg	Glu	Asp	Glu	Leu	Val	Arg	
			180					185					190			
tca	ttg	acc	cta	gct	tac	aaa	cgc	caa	aca	ctc	aaa	gac	aga	ctc	tat	624
Ser	Leu	Thr	Leu	Ala	Tyr	Lys	Arg	Gln	Thr	Leu	Lys	Asp	Arg	Leu	Tyr	
		195					200					205				
gat	tta	gaa	cct	acc	agc	aaa	ctg	att	aat	gaa	tta	gtc	aaa	acg	atg	672
Asp	Leu	Glu	Pro	Thr	Ser	Lys	Leu	Ile	Asn	Glu	Leu	Val	Lys	Thr	Met	
		210				215					220					
gaa	acc	act	tta	aaa	agc	ggc	gat	ggg	ttt	gaa	aaa	gag	ttg	aaa	cgc	720
Glu	Thr	Thr	Leu	Lys	Ser	Gly	Asp	Gly	Phe	Glu	Lys	Glu	Leu	Lys	Arg	
225					230					235					240	
ttg	gaa	tac	aaa	ctg	ccc	tta	ttc	aat	gac	act	ctc	atc	gca	aac	cat	768
Leu	Glu	Tyr	Lys	Leu	Pro	Leu	Phe	Asn	Asp	Thr	Leu	Ile	Ala	Asn	His	
			245						250					255		
aaa	aaa	atc	ctt	gcc	aat	atc	act	aac	atg	act	aaa	gaa	gat	att	atc	816
Lys	Lys	Ile	Leu	Ala	Asn	Ile	Thr	Asn	Met	Thr	Lys	Glu	Asp	Ile	Ile	
			260					265				270				
gct	caa	gtg	cca	gaa	gcg	act	atg	gtg	agc	gtg	tat	atg	gat	ctt	aaa	864
Ala	Gln	Val	Pro	Glu	Ala	Thr	Met	Val	Ser	Val	Tyr	Met	Asp	Leu	Lys	
		275					280					285				
aag	ctt	ttt	ttg	act	aaa	gaa	gcg	agc	gaa	gaa	ggc	ttt	gat	cta	gcc	912
Lys	Leu	Phe	Leu	Thr	Lys	Glu	Ala	Ser	Glu	Glu	Gly	Phe	Asp	Leu	Ala	
		290				295					300					
ccc	aac	aag	cta	aaa	gaa	att	tta	gag	caa	atc	aaa	aga	ggg	aag	ttg	960
Pro	Asn	Lys	Leu	Lys	Glu	Ile	Leu	Glu	Gln	Ile	Lys	Arg	Gly	Lys	Leu	
305					310					315					320	
att	tcc	gat	cgc	gct	aaa	aac	aaa	atg	gct	aaa	tcc	aat	tta	agg	ttg	1008
Ile	Ser	Asp	Arg	Ala	Lys	Asn	Lys	Met	Ala	Lys	Ser	Asn	Leu	Arg	Leu	
			325						330					335		
gtg	gtg	agc	atc	gct	aaa	cga	ttc	acg	agc	aga	ggc	tta	cca	ttc	ttg	1056
Val	Val	Ser	Ile	Ala	Lys	Arg	Phe	Thr	Ser	Arg	Gly	Leu	Pro	Phe	Leu	
			340					345					350			
gat	ttg	att	caa	gag	ggc	aat	att	ggc	ttg	atg	aaa	gcg	gtg	gat	aag	1104
Asp	Leu	Ile	Gln	Glu	Gly	Asn	Ile	Gly	Leu	Met	Lys	Ala	Val	Asp	Lys	
		355				360					365					
ttt	gag	cat	gaa	aag	ggc	ttc	aag	ttt	tct	acc	tat	gcg	acc	tgg	tgg	1152
Phe	Glu	His	Glu	Lys	Gly	Phe	Lys	Phe	Ser	Thr	Tyr	Ala	Thr	Trp	Trp	
		370				375					380					
atc	aaa	caa	gct	atc	agc	aga	gcc	ata	gcc	gat	cag	gcc	cgc	act	atc	1200
Ile	Lys	Gln	Ala	Ile	Ser	Arg	Ala	Ile	Ala	Asp	Gln	Ala	Arg	Thr	Ile	
385					390					395					400	
cgc	atc	ccc	att	cac	atg	att	gat	acg	att	aat	cgc	atc	aat	aaa	gtc	1248
Arg	Ile	Pro	Ile	His	Met	Ile	Asp	Thr	Ile	Asn	Arg	Ile	Asn	Lys	Val	
				405					410					415		
atg	cgc	aaa	cac	att	caa	gaa	aac	ggc	aaa	gag	cct	gat	tta	gaa	gtg	1296
Met	Arg	Lys	His	Ile	Gln	Glu	Asn	Gly	Lys	Glu	Pro	Asp	Leu	Glu	Val	

420 425 430
 gtg gct gaa gaa gtg ggg ctt tcg tta gat aaa gtg aag aat gtg att 1344
 Val Ala Glu Glu Val Gly Leu Ser Leu Asp Lys Val Lys Asn Val Ile
 435 440 445
 aag gtg act aaa gag cct atc agt ttg gaa acc cca gtc ggc aat gat 1392
 Lys Val Thr Lys Glu Pro Ile Ser Leu Glu Thr Pro Val Gly Asn Asp
 450 455 460
 gat gat ggc aag ttt ggg gat ttc gtg gaa gat aag aat atc gtc agc 1440
 Asp Asp Gly Lys Phe Gly Asp Phe Val Glu Asp Lys Asn Ile Val Ser
 465 470 475 480
 tcc att gat cac atc atg cga gaa gat ttg aaa gca caa att gaa agc 1488
 Ser Ile Asp His Ile Met Arg Glu Asp Leu Lys Ala Gln Ile Glu Ser
 485 490 495
 gtt ttg gat cag ttg aat gag cga gaa aaa gcg gtg atc cgc atg cgt 1536
 Val Leu Asp Gln Leu Asn Glu Arg Glu Lys Ala Val Ile Arg Met Arg
 500 505 510
 ttt ggg ctt tta gac gat gaa agc gat cga act tta gaa gaa att ggc 1584
 Phe Gly Leu Leu Asp Asp Glu Ser Asp Arg Thr Leu Glu Glu Ile Gly
 515 520 525
 aag gaa ttg aat gtt act aga gaa agg gtg cgc cag att gaa agc tct 1632
 Lys Glu Leu Asn Val Thr Arg Glu Arg Val Arg Gln Ile Glu Ser Ser
 530 535 540
 gcg att aaa aaa ttg aga agc ccg cag tac ggg cgc att tta aga aac 1680
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 Tyr Leu Arg Ile
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 35 40 45
 Ser Asp Ser Pro Val Arg Met Tyr Leu Arg Glu Met Gly Asp Ile Lys
 50 55 60
 Leu Leu Ser Lys Asp Glu Glu Ile Glu Leu Ser Lys Gln Ile Arg Leu
 65 70 75 80
 Gly Glu Asp Ile Ile Leu Asp Ala Ile Cys Ser Val Pro Tyr Leu Ile
 85 90 95
 Asp Phe Ile Tyr Ala Tyr Lys Asp Ala Leu Ile Asn Arg Glu Arg Arg
 100 105 110
 Val Lys Glu Leu Phe Arg Ser Phe Asp Asp Asp Asp Glu Asn Ser Val
 115 120 125
 Ser Asp Ser Lys Lys Asp Glu Asp Asn Glu Glu Asp Glu Glu Asn Glu
 130 135 140
 Glu Arg Lys Lys Val Val Ser Glu Lys Asp Lys Lys Arg Val Glu Lys
 145 150 155 160
 Val Gln Glu Ser Phe Lys Ala Leu Asp Lys Ala Lys Lys Glu Trp Leu
 165 170 175
 Lys Ala Leu Glu Ala Pro Ile Asp Glu Arg Glu Asp Glu Leu Val Arg
 180 185 190
 Ser Leu Thr Leu Ala Tyr Lys Arg Gln Thr Leu Lys Asp Arg Leu Tyr
 195 200 205
 Asp Leu Glu Pro Thr Ser Lys Leu Ile Asn Glu Leu Val Lys Thr Met
 210 215 220
 Glu Thr Thr Leu Lys Ser Gly Asp Gly Phe Glu Lys Glu Leu Lys Arg

225 230 235 240
 Leu Glu Tyr Lys Leu Pro Leu Phe Asn Asp Thr Leu Ile Ala Asn His
 245 250 255
 Lys Lys Ile Leu Ala Asn Ile Thr Asn Met Thr Lys Glu Asp Ile Ile
 260 265 270
 Ala Gln Val Pro Glu Ala Thr Met Val Ser Val Tyr Met Asp Leu Lys
 275 280 285
 Lys Leu Phe Leu Thr Lys Glu Ala Ser Glu Glu Gly Phe Asp Leu Ala
 290 295 300
 Pro Asn Lys Leu Lys Glu Ile Leu Glu Gln Ile Lys Arg Gly Lys Leu
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 Ile Ser Asp Arg Ala Lys Asn Lys Met Ala Lys Ser Asn Leu Arg Leu
 325 330 335
 Val Val Ser Ile Ala Lys Arg Phe Thr Ser Arg Gly Leu Pro Phe Leu
 340 345 350
 Asp Leu Ile Gln Glu Gly Asn Ile Gly Leu Met Lys Ala Val Asp Lys
 355 360 365
 Phe Glu His Glu Lys Gly Phe Lys Phe Ser Thr Tyr Ala Thr Trp Trp
 370 375 380
 Ile Lys Gln Ala Ile Ser Arg Ala Ile Ala Asp Gln Ala Arg Thr Ile
 385 390 395
 Arg Ile Pro Ile His Met Ile Asp Thr Ile Asn Arg Ile Asn Lys Val
 405 410 415
 Met Arg Lys His Ile Gln Glu Asn Gly Lys Glu Pro Asp Leu Glu Val
 420 425 430
 Val Ala Glu Glu Val Gly Leu Ser Leu Asp Lys Val Lys Asn Val Ile
 435 440 445
 Lys Val Thr Lys Glu Pro Ile Ser Leu Glu Thr Pro Val Gly Asn Asp
 450 455 460
 Asp Asp Gly Lys Phe Gly Asp Phe Val Glu Asp Lys Asn Ile Val Ser
 465 470 475
 Ser Ile Asp His Ile Met Arg Glu Asp Leu Lys Ala Gln Ile Glu Ser
 485 490 495
 Val Leu Asp Gln Leu Asn Glu Arg Glu Lys Ala Val Ile Arg Met Arg
 500 505 510
 Phe Gly Leu Leu Asp Asp Glu Ser Asp Arg Thr Leu Glu Glu Ile Gly
 515 520 525
 Lys Glu Leu Asn Val Thr Arg Glu Arg Val Arg Gln Ile Glu Ser Ser
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Tyr Leu Arg Ile

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<211> 237

<212> DNA

<213> Helicobacter pylori

<220>

<221> CDS

<222> (1)..(237)

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gaa tta gag gat ttg tat cac gaa ttc agt gaa gat aag cgt tct att 96

Glu Leu Glu Asp Leu Tyr His Glu Phe Ser Glu Asp Lys Arg Ser Ile

20 25 30

ttc tat ttt gcc ccc aca aac gcc cac aaa gac atg ctc aaa gcg gtg 144

Phe Tyr Phe Ala Pro Thr Asn Ala His Lys Asp Met Leu Lys Ala Val

35 40 45

gat ttt ttc aaa gaa aaa ggt cat acg gct tat tta gat gag gtg agg 192

Asp Phe Phe Lys Glu Lys Gly His Thr Ala Tyr Leu Asp Glu Val Arg

50 55 60
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 20 25 30
 Phe Tyr Phe Ala Pro Thr Asn Ala His Lys Asp Met Leu Lys Ala Val
 35 40 45
 Asp Phe Phe Lys Glu Lys Gly His Thr Ala Tyr Leu Asp Glu Val Arg
 50 55 60
 Val Ser Thr Asp Glu Lys Asp Phe Leu Tyr Glu Leu His Ile Ile
 65 70 75
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 1 5 10 15
 gaa tac aaa acc tta gag cct tta aaa agc cta gaa atc cgt ttg agt 96
 Glu Tyr Lys Thr Leu Glu Pro Leu Lys Ser Leu Glu Ile Arg Leu Ser
 20 25 30
 gaa gcc ccc att gat aaa cgc aat gat ttt tta tac cat aag acc act 144
 Glu Ala Pro Ile Asp Lys Arg Asn Asp Phe Leu Tyr His Lys Thr Thr
 35 40 45
 tat gcc cct ttt tat caa aag gct cga gcg ctc att aaa aag ggc gtt 192
 Tyr Ala Pro Phe Tyr Gln Lys Ala Arg Ala Leu Ile Lys Lys Gly Val
 50 55 60
 atg ttt gat gaa atc ttt tat aac cag gat ttg gaa ctc act gag ggc 240
 Met Phe Asp Glu Ile Phe Tyr Asn Gln Asp Leu Glu Leu Thr Glu Gly
 65 70 75 80
 gct agg agc aat ctt gtt tta gaa atc cat aac agg ctt tta acc cct 288
 Ala Arg Ser Asn Leu Val Leu Glu Ile His Asn Arg Leu Leu Thr Pro
 85 90 95
 tat ttt agc gcg ggc gcg tta aac ggg acg ggt gtt gtg ggg ttg tta 336
 Tyr Phe Ser Ala Gly Ala Leu Asn Gly Thr Gly Val Val Gly Leu Leu
 100 105 110
 aaa aag ggt ctt gtt ggg cat gca cct ttg aaa ttg caa gat ttg caa 384
 Lys Lys Gly Leu Val Gly His Ala Pro Leu Lys Leu Gln Asp Leu Gln
 115 120 125
 aaa gcg tct aaa atc tat tgt att aac gcg cta tat ggc tta gtg gaa 432
 Lys Ala Ser Lys Ile Tyr Cys Ile Asn Ala Leu Tyr Gly Leu Val Glu
 130 135 140
 gtg aaa ata aaa 444
 Val Lys Ile Lys
 145
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 <211> 148
 <212> PRT
 <213> *Helicobacter pylori*

<400> 94
 Glu Gly Val Leu Arg Val Leu Leu Asn Lys Lys Gly Lys Leu Ile Lys
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 Glu Tyr Lys Thr Leu Glu Pro Leu Lys Ser Leu Glu Ile Arg Leu Ser
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 Glu Ala Pro Ile Asp Lys Arg Asn Asp Phe Leu Tyr His Lys Thr Thr
 35 40 45
 Tyr Ala Pro Phe Tyr Gln Lys Ala Arg Ala Leu Ile Lys Lys Gly Val
 50 55 60
 Met Phe Asp Glu Ile Phe Tyr Asn Gln Asp Leu Glu Leu Thr Glu Gly
 65 70 75 80
 Ala Arg Ser Asn Leu Val Leu Glu Ile His Asn Arg Leu Leu Thr Pro
 85 90 95
 Tyr Phe Ser Ala Gly Ala Leu Asn Gly Thr Gly Val Val Gly Leu Leu
 100 105 110
 Lys Lys Gly Leu Val Gly His Ala Pro Leu Lys Leu Gln Asp Leu Gln
 115 120 125
 Lys Ala Ser Lys Ile Tyr Cys Ile Asn Ala Leu Tyr Gly Leu Val Glu
 130 135 140
 Val Lys Ile Lys
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<211> 719

<212> DNA

<213> Helicobacter pylori

<220>

<221> CDS

<222> (1)..(717)

<400> 95

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 1 5 10 15
 aaa ata gat tgg caa aaa gat tat gac agg gaa aaa tta gaa cga gat 96
 Lys Ile Asp Trp Gln Lys Asp Tyr Asp Arg Glu Lys Leu Glu Arg Asp
 20 25 30
 aat agg gat tta gaa caa tgc aaa gag gat tta tta gcc gct aac gag 144
 Asn Arg Asp Leu Glu Gln Cys Lys Glu Asp Leu Leu Ala Ala Asn Glu
 35 40 45
 aat cta aga aat aga atc caa gaa tgg gaa aat gaa aaa aac aag ctt 192
 Asn Leu Arg Asn Arg Ile Gln Glu Trp Glu Asn Glu Lys Asn Lys Leu
 50 55 60
 gat cca aga gat gaa aga ata aaa gag tta gaa gaa gaa aaa agg gaa 240
 Asp Pro Arg Asp Glu Arg Ile Lys Glu Leu Glu Glu Glu Lys Arg Glu
 65 70 75 80
 tta gag gga att tta gcc caa aaa gag aac gca gaa caa aaa tat aac 288
 Leu Glu Gly Ile Leu Ala Gln Lys Glu Asn Ala Glu Gln Lys Tyr Asn
 85 90 95
 act ctt tca gtc aaa aat aag caa tta gaa gct gag tta gat atg ctt 336
 Thr Leu Ser Val Lys Asn Lys Gln Leu Glu Ala Glu Leu Asp Met Leu
 100 105 110
 aac gaa aaa ttt gaa aaa ctg aaa aat atg tat gct ggg gta gag gat 384
 Asn Glu Lys Phe Glu Lys Leu Lys Asn Met Tyr Ala Gly Val Glu Asp
 115 120 125
 ttt gaa aaa cgc caa aaa aat atc aaa gaa caa att gta aaa acc aac 432
 Phe Glu Lys Arg Gln Lys Asn Ile Lys Glu Gln Ile Val Lys Thr Asn
 130 135 140
 ccc aaa gtc tta ggc gca cct tca aac gaa gtg gaa gaa tta gcg ttc 480
 Pro Lys Val Leu Gly Ala Pro Ser Asn Glu Val Glu Glu Leu Ala Phe
 45 150 155 160
 tta gag cgt ata gaa aag ggc atg caa gag ttc aat gtt ttc tat ccc 528
 Leu Glu Arg Ile Glu Lys Gly Met Gln Glu Phe Asn Val Phe Tyr Pro


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          165          170          175
aag cgt tta ttg tat atg ttc cac acc gct tta aaa agc acg tct cta 576
Lys Arg Leu Leu Tyr Met Phe His Thr Ala Leu Lys Ser Thr Ser Leu
          180          185          190
tcg cca ttg agc gtg cta agt ggg gtg agt ggg aca gga aaa tct gaa 624
Ser Pro Leu Ser Val Leu Ser Gly Val Ser Gly Thr Gly Lys Ser Glu
          195          200          205
ctg ccc aag ctc tat gtg cat ttt ggg ggg tta aat ttt tta agc att 672
Leu Pro Lys Leu Tyr Val His Phe Gly Gly Leu Asn Phe Leu Ser Ile
          210          215          220
gct gtg cag cct act tgg gat agc cca gaa tcg ttg atg ggg tat tt 719
Ala Val Gln Pro Thr Trp Asp Ser Pro Glu Ser Leu Met Gly Tyr
          225          230          235

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<210> 96

<211> 239

<212> PRT

<213> *Helicobacter pylori*

<400> 96

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Ala Asp Glu Thr Asn Ala Leu Arg Gln Lys Asn Arg Glu Leu Asn Lys
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Lys Ile Asp Trp Gln Lys Asp Tyr Asp Arg Glu Lys Leu Glu Arg Asp
          20          25          30
Asn Arg Asp Leu Glu Gln Cys Lys Glu Asp Leu Leu Ala Ala Asn Glu
          35          40          45
Asn Leu Arg Asn Arg Ile Gln Glu Trp Glu Asn Glu Lys Asn Lys Leu
          50          55          60
Asp Pro Arg Asp Glu Arg Ile Lys Glu Leu Glu Glu Lys Arg Glu
          65          70          75          80
Leu Glu Gly Ile Leu Ala Gln Lys Glu Asn Ala Glu Gln Lys Tyr Asn
          85          90          95
Thr Leu Ser Val Lys Asn Lys Gln Leu Glu Ala Glu Leu Asp Met Leu
          100          105          110
Asn Glu Lys Phe Glu Lys Leu Lys Asn Met Tyr Ala Gly Val Glu Asp
          115          120          125
Phe Glu Lys Arg Gln Lys Asn Ile Lys Glu Gln Ile Val Lys Thr Asn
          130          135          140
Pro Lys Val Leu Gly Ala Pro Ser Asn Glu Val Glu Glu Leu Ala Phe
          145          150          155          160
Leu Glu Arg Ile Glu Lys Gly Met Gln Glu Phe Asn Val Phe Tyr Pro
          165          170          175
Lys Arg Leu Leu Tyr Met Phe His Thr Ala Leu Lys Ser Thr Ser Leu
          180          185          190
Ser Pro Leu Ser Val Leu Ser Gly Val Ser Gly Thr Gly Lys Ser Glu
          195          200          205
Leu Pro Lys Leu Tyr Val His Phe Gly Gly Leu Asn Phe Leu Ser Ile
          210          215          220
Ala Val Gln Pro Thr Trp Asp Ser Pro Glu Ser Leu Met Gly Tyr
          225          230          235

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<210> 97

<211> 819

<212> DNA

<213> *Helicobacter pylori*

<220>

<221> CDS

<222> (1)..(819)

<400> 97

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  1          5          10          15
tta gat caa gcc ccc ata ggc aaa acc cca cga agc aac cct gcc act 96
Leu Asp Gln Ala Pro Ile Gly Lys Thr Pro Arg Ser Asn Pro Ala Thr

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	20	25	30	
tac acg gga gtg atg gat gaa atc agg att tta ttt gcc gag caa aaa				144
Tyr Thr Gly Val Met Asp Glu Ile Arg Ile Leu Phe Ala Glu Gln Lys				
	35	40	45	
gaa gct aaa att tta ggc tat agt gcg agc cgt ttt agc ttt aat gtt				192
Glu Ala Lys Ile Leu Gly Tyr Ser Ala Ser Arg Phe Ser Phe Asn Val				
	50	55	60	
aaa gga ggg cgg tgc gag aaa tgc caa ggc gat ggg gac att aaa ata				240
Lys Gly Gly Arg Cys Glu Lys Cys Gln Gly Asp Gly Asp Ile Lys Ile				
	65	70	75	80
gaa atg cac ttt ttg cct gat gtg tta gtc caa tgc gat agc tgt aag				288
Glu Met His Phe Leu Pro Asp Val Leu Val Gln Cys Asp Ser Cys Lys				
	85	90	95	
ggc gct aaa tac aac ccc caa act tta gaa atc aag gtg aaa ggc aaa				336
Gly Ala Lys Tyr Asn Pro Gln Thr Leu Glu Ile Lys Val Lys Gly Lys				
	100	105	110	
tcc att gcc gat gtg ttg aac atg agc gtg/gaa gag gct tat gaa ttt				384
Ser Ile Ala Asp Val Leu Asn Met Ser Val Glu Glu Ala Tyr Glu Phe				
	115	120	125	
ttt gct aaa ttc cct aaa atc gcc gtg aag tta aaa acg ctt atg gat				432
Phe Ala Lys Phe Pro Lys Ile Ala Val Lys Leu Lys Thr Leu Met Asp				
	130	135	140	
gtg ggc tta ggc tat atc act tta ggg caa aac gct acg act tta agt				480
Val Gly Leu Gly Tyr Ile Thr Leu Gly Gln Asn Ala Thr Thr Leu Ser				
	145	150	155	160
ggg ggg gag gct caa agg atc aaa tta gct aaa gaa ttg agt aaa aaa				528
Gly Gly Glu Ala Gln Arg Ile Lys Leu Ala Lys Glu Leu Ser Lys Lys				
	165	170	175	
gac aca ggc aaa acc ctt tat att tta gat gag cct act acc ggt ttg				576
Asp Thr Gly Lys Thr Leu Tyr Ile Leu Asp Glu Pro Thr Thr Gly Leu				
	180	185	190	
cat ttt gaa gac gtg aat cat ctt tta caa gtc ttg cat tct tta gtg				624
His Phe Glu Asp Val Asn His Leu Leu Gln Val Leu His Ser Leu Val				
	195	200	205	
gcg tta ggc aat tct atg cta gtg att gag cat aat tta gac att atc				672
Ala Leu Gly Asn Ser Met Leu Val Ile Glu His Asn Leu Asp Ile Ile				
	210	215	220	
aaa aac gct gac tac att ata gac atg ggg cct gat ggg ggg gat aag				720
Lys Asn Ala Asp Tyr Ile Ile Asp Met Gly Pro Asp Gly Gly Asp Lys				
	225	230	235	240
ggc ggg aaa gtc att gcg agc ggc acg cct tta gag gtg gcg caa aat				768
Gly Gly Lys Val Ile Ala Ser Gly Thr Pro Leu Glu Val Ala Gln Asn				
	245	250	255	
tgc gaa aaa acc caa agc tac acg gga aaa ttt tta gct ttg gaa ttg				816
Cys Glu Lys Thr Gln Ser Tyr Thr Gly Lys Phe Leu Ala Leu Glu Leu				
	260	265	270	
aaa				819
Lys				
<210> 98				
<211> 273				
<212> PRT				
<213> Helicobacter pylori				
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20 25 30				
Tyr Thr Gly Val Met Asp Glu Ile Arg Ile Leu Phe Ala Glu Gln Lys				
35 40 45				
Glu Ala Lys Ile Leu Gly Tyr Ser Ala Ser Arg Phe Ser Phe Asn Val				
50 55 60				

Lys Gly Gly Arg Cys Glu Lys Cys Gln Gly Asp Gly Asp Ile Lys Ile
 65 70 75 80
 Glu Met His Phe Leu Pro Asp Val Leu Val Gln Cys Asp Ser Cys Lys
 85 90 95
 Gly Ala Lys Tyr Asn Pro Gln Thr Leu Glu Ile Lys Val Lys Gly Lys
 100 105 110
 Ser Ile Ala Asp Val Leu Asn Met Ser Val Glu Glu Ala Tyr Glu Phe
 115 120 125
 Phe Ala Lys Phe Pro Lys Ile Ala Val Lys Leu Lys Thr Leu Met Asp
 130 135 140
 Val Gly Leu Gly Tyr Ile Thr Leu Gly Gln Asn Ala Thr Thr Leu Ser
 145 150 155 160
 Gly Gly Glu Ala Gln Arg Ile Lys Leu Ala Lys Glu Leu Ser Lys Lys
 165 170 175
 Asp Thr Gly Lys Thr Leu Tyr Ile Leu Asp Glu Pro Thr Thr Gly Leu
 180 185 190
 His Phe Glu Asp Val Asn His Leu Gln Val Leu His Ser Leu Val
 195 200 205
 Ala Leu Gly Asn Ser Met Leu Val Ile Glu His Asn Leu Asp Ile Ile
 210 215 220
 Lys Asn Ala Asp Tyr Ile Ile Asp Met Gly Pro Asp Gly Gly Asp Lys
 225 230 235 240
 Gly Gly Lys Val Ile Ala Ser Gly Thr Pro Leu Glu Val Ala Gln Asn
 245 250 255
 Cys Glu Lys Thr Gln Ser Tyr Thr Gly Lys Phe Leu Ala Leu Glu Leu
 260 265 270

Lys

<210> 99

<211> 1405

<212> DNA

<213> *Helicobacter pylori*

<220>

<221> CDS

<222> (1)..(1404)

<400> 99

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 ggt ggc att gaa atc tta agg act tta att gat ttt acg ccc aaa att 96
 Gly Gly Ile Glu Ile Leu Arg Thr Leu Ile Asp Phe Thr Pro Lys Ile
 20 25 30
 gaa aac gcc ctg aat tta gcg gcc aaa agc cat aag ggg caa tac aga 144
 Glu Asn Ala Leu Asn Leu Ala Ala Lys Ser His Lys Gly Gln Tyr Arg
 35 40 45
 aaa agc ggc gag cct tat att gtc cat cct att tgc gtg gca agc ttg 192
 Lys Ser Gly Glu Pro Tyr Ile Val His Pro Ile Cys Val Ala Ser Leu
 50 55 60
 gta gcg ttt tgt ggg ggc gat gag gcg atg gtg tgt gct gcg ctt ttg 240
 Val Ala Phe Cys Gly Gly Asp Glu Ala Met Val Cys Ala Ala Leu Leu
 65 70 75 80
 cat gat gtg gtg gaa gac acg cct tgt aag att gaa acg att gag caa 288
 His Asp Val Val Glu Asp Thr Pro Cys Lys Ile Glu Thr Ile Glu Gln
 85 90 95
 gaa ttt ggg caa gat gtg gct aat tta gtg gat gcg ctc act aaa atc 336
 Glu Phe Gly Gln Asp Val Ala Asn Leu Val Asp Ala Leu Thr Lys Ile
 100 105 110
 act gaa atc agg aaa gaa gaa tta ggc gtg agc tct caa gat ccc aga 384
 Thr Glu Ile Arg Lys Glu Glu Leu Gly Val Ser Ser Gln Asp Pro Arg
 115 120 125
 atg gtg gtt tca gcg ctc act ttc aga aag att tta att agc gcg ata 432
 Met Val Val Ser Ala Leu Thr Phe Arg Lys Ile Leu Ile Ser Ala Ile

130	caa gat cca aga gcc tta gtg gta aag att agc gac agg ttg cac aac	135	140	480
Gln Asp Pro Arg Ala	Leu Val Val Lys Ile Ser Asp Arg Leu His Asn	150	155	160
145	atg ctc acc tta gac gcc ttg cct cat gac aag caa gtg cgt att tct	165	170	175
Met Leu Thr Leu Asp Ala Leu Pro His Asp Lys Gln Val Arg Ile Ser	180	185	190	528
aaa gag act cta gcg gtg tat gcc cct ata gcg agc cga ttg ggc atg	Lys Glu Thr Leu Ala Val Tyr Ala Pro Ile Ala Ser Arg Leu Gly Met	195	200	205
tct tca atc aaa aat gaa tta gaa gac aag agc ttt tat tat att tat	Ser Ser Ile Lys Asn Glu Leu Glu Asp Lys Ser Phe Tyr Tyr Ile Tyr	210	215	220
cca gaa gag tat aaa aat atc aag gaa tat ttg cac aaa aac aag cag	Pro Glu Glu Tyr Lys Asn Ile Lys Glu Tyr Leu His Lys Asn Lys Gln	225	230	235
tct tta ctc tta aag ctc aac gct ttt gcg agc aag tta gaa aaa aaa	Ser Leu Leu Leu Lys Leu Asn Ala Phe Ala Ser Lys Leu Glu Lys Lys	240	245	250
ctt ttt gat agt ggg ttt agc cat tcg gat ttt aaa ctc gtt aca agg	Leu Phe Asp Ser Gly Phe Ser His Ser Asp Phe Lys Leu Val Thr Arg	255	260	265
gtg aaa cgc cct tat tct atc tat ctt aag atg caa cga aag ggc gcg	Val Lys Arg Pro Tyr Ser Ile Tyr Leu Lys Met Gln Arg Lys Gly Ala	270	275	280
gtt aat att gat gaa att ttg gac ttg tta gcc att agg att tta ttg	Val Asn Ile Asp Glu Ile Leu Asp Leu Leu Ala Ile Arg Ile Leu Leu	285	290	295
aaa aac ccg att gat tgc tat aaa gtt tta ggg att atc cat ttg aat	Lys Asn Pro Ile Asp Cys Tyr Lys Val Leu Gly Ile Ile His Leu Asn	300	305	310
ttc aaa ccc att gtc tct cgt ttt aaa gat tac atc gct ttg ccc aaa	Phe Lys Pro Ile Val Ser Arg Phe Lys Asp Tyr Ile Ala Leu Pro Lys	315	320	325
gaa aat ggc tat aag acg ata cac acg acc att ttt gat gaa tct tct	Glu Asn Gly Tyr Lys Thr Ile His Thr Thr Ile Phe Asp Glu Ser Ser	330	335	340
gtt tat gaa gtg cag atc cgc acc ttt gat atg cat atg ggg gcg gag	Val Tyr Glu Val Gln Ile Arg Thr Phe Asp Met His Met Gly Ala Glu	345	350	355
tat ggt aat tca gcc cac tgg aag tat aaa gcc ggg ggc gtg gat cat	Tyr Gly Asn Ser Ala His Trp Lys Tyr Lys Ala Gly Gly Val Asp His	360	365	370
gaa gat cat cat gag ggc atg aga tgg ttg caa aat ttt aaa tac cat	Glu Asp His His Glu Gly Met Arg Trp Leu Gln Asn Phe Lys Tyr His	375	380	385
gac agc gat ttg aaa aac gac cct aag gaa ttt tac gaa ctc gct aag	Asp Ser Asp Leu Lys Asn Asp Pro Lys Glu Phe Tyr Glu Leu Ala Lys	390	395	400
aac gat ttg tat cgt gaa gat att gtc gtt ttt tcg cct cat ggg gac	Asn Asp Leu Tyr Arg Glu Asp Ile Val Val Phe Ser Pro His Gly Asp	405	410	415
act tac act tta ccg gtg ggt gcg atc gct tta gat ttt gct tac atg	Thr Tyr Thr Leu Pro Val Gly Ala Ile Ala Leu Asp Phe Ala Tyr Met	420	425	430
gtg cat agc gat ttg ggc gat aaa gcc acg gac gct tat atc aat agt	Val His Ser Asp Leu Gly Asp Lys Ala Thr Asp Ala Tyr Ile Asn Ser	435	440	445
aaa aaa gcc tta ctc aat cag gaa tta aga agt ggg gat gtg gtt aaa	Lys Lys Ala Leu Leu Asn Gln Glu Leu Arg Ser Gly Asp Val Val Lys	450	455	460

1405

atc att aaa ggc g

Ile Ile Lys Gly

465

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<211> 468

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 20 25 30
 Glu Asn Ala Leu Asn Leu Ala Ala Lys Ser His Lys Gly Gln Tyr Arg
 35 40 45
 Lys Ser Gly Glu Pro Tyr Ile Val His Pro Ile Cys Val Ala Ser Leu
 50 55 60
 Val Ala Phe Cys Gly Gly Asp Glu Ala Met Val Cys Ala Ala Leu Leu
 65 70 75 80
 His Asp Val Val Glu Asp Thr Pro Cys Lys Ile Glu Thr Ile Glu Gln
 85 90 95
 Glu Phe Gly Gln Asp Val Ala Asn Leu Val Asp Ala Leu Thr Lys Ile
 100 105 110
 Thr Glu Ile Arg Lys Glu Glu Leu Gly Val Ser Ser Gln Asp Pro Arg
 115 120 125
 Met Val Val Ser Ala Leu Thr Phe Arg Lys Ile Leu Ile Ser Ala Ile
 130 135 140
 Gln Asp Pro Arg Ala Leu Val Val Lys Ile Ser Asp Arg Leu His Asn
 145 150 155 160
 Met Leu Thr Leu Asp Ala Leu Pro His Asp Lys Gln Val Arg Ile Ser
 165 170 175
 Lys Glu Thr Leu Ala Val Tyr Ala Pro Ile Ala Ser Arg Leu Gly Met
 180 185 190
 Ser Ser Ile Lys Asn Glu Leu Glu Asp Lys Ser Phe Tyr Tyr Ile Tyr
 195 200 205
 Pro Glu Glu Tyr Lys Asn Ile Lys Glu Tyr Leu His Lys Asn Lys Gln
 210 215 220
 Ser Leu Leu Leu Lys Leu Asn Ala Phe Ala Ser Lys Leu Glu Lys Lys
 225 230 235 240
 Leu Phe Asp Ser Gly Phe Ser His Ser Asp Phe Lys Leu Val Thr Arg
 245 250 255
 Val Lys Arg Pro Tyr Ser Ile Tyr Leu Lys Met Gln Arg Lys Gly Ala
 260 265 270
 Val Asn Ile Asp Glu Ile Leu Asp Leu Leu Ala Ile Arg Ile Leu Leu
 275 280 285
 Lys Asn Pro Ile Asp Cys Tyr Lys Val Leu Gly Ile Ile His Leu Asn
 290 295 300
 Phe Lys Pro Ile Val Ser Arg Phe Lys Asp Tyr Ile Ala Leu Pro Lys
 305 310 315 320
 Glu Asn Gly Tyr Lys Thr Ile His Thr Thr Ile Phe Asp Glu Ser Ser
 325 330 335
 Val Tyr Glu Val Gln Ile Arg Thr Phe Asp Met His Met Gly Ala Glu
 340 345 350
 Tyr Gly Asn Ser Ala His Trp Lys Tyr Lys Ala Gly Gly Val Asp His
 355 360 365
 Glu Asp His His Glu Gly Met Arg Trp Leu Gln Asn Phe Lys Tyr His
 370 375 380
 Asp Ser Asp Leu Lys Asn Asp Pro Lys Glu Phe Tyr Glu Leu Ala Lys
 385 390 395 400
 Asn Asp Leu Tyr Arg Glu Asp Ile Val Val Phe Ser Pro His Gly Asp
 405 410 415
 Thr Tyr Thr Leu Pro Val Gly Ala Ile Ala Leu Asp Phe Ala Tyr Met

420 425 430
 Val His Ser Asp Leu Gly Asp Lys Ala Thr Asp Ala Tyr Ile Asn Ser
 435 440 445
 Lys Lys Ala Leu Leu Asn Gln Glu Leu Arg Ser Gly Asp Val Val Lys
 450 455 460
 Ile Ile Lys Gly
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 Pro Lys Glu Arg Val Leu Ser Asp Glu Glu Ile Asn Asn Arg Ala Glu
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 agg atc gct aaa agc gag tta gag aag gat acg aag ctc gtt tca tca 96
 Arg Ile Ala Lys Ser Glu Leu Glu Lys Asp Thr Lys Leu Val Ser Ser
 20 25 30
 cac gat caa tac gag cgc atg aaa aaa agc gga tcg ctc aac acg gaa 144
 His Asp Gln Tyr Glu Arg Met Lys Lys Ser Gly Ser Leu Asn Thr Glu
 35 40 45
 aac tta gat tcg cac att caa gcc aac agc tta caa gag ctg aat caa 192
 Asn Leu Asp Ser His Ile Gln Ala Asn Ser Leu Gln Glu Leu Asn Gln
 50 55 60
 aaa ttg ctc caa ttc gtg ggc gcg gat agg aag tat atg ccc tac act 240
 Lys Leu Leu Gln Phe Val Gly Ala Asp Arg Lys Tyr Met Pro Tyr Thr
 65 70 75 80
 aaa gcg gtg caa att tct ttg aat aac ccc aat ctt aaa gat ttg gaa 288
 Lys Ala Val Gln Ile Ser Leu Asn Asn Pro Asn Leu Lys Asp Leu Glu
 85 90 95
 gtg att gac acc cca gga gtg aat gac ccc atc gct tcc agg gaa gaa 336
 Val Ile Asp Thr Pro Gly Val Asn Asp Pro Ile Ala Ser Arg Glu Glu
 100 105 110
 cgc acc aaa gcc tta ttg aaa gat tgc gat gtg gtg ttt atc ata agc 384
 Arg Thr Lys Ala Leu Leu Lys Asp Cys Asp Val Val Phe Ile Ile Ser
 115 120 125
 tct tct aat cag ttt tta acg gag agc gat atg agt ttg ttt gac agg 432
 Ser Ser Asn Gln Phe Leu Thr Glu Ser Asp Met Ser Leu Phe Asp Arg
 130 135 140
 gtt tct aac aaa gaa agc ctt caa gaa att tat ttt gtg gca agc caa 480
 Val Ser Asn Lys Glu Ser Leu Gln Glu Ile Tyr Phe Val Ala Ser Gln
 145 150 155 160
 gcc gat agc gct gtt ctt tct atg agt gaa gtg gaa aaa tct cgc cac 528
 Ala Asp Ser Ala Val Leu Ser Met Ser Glu Val Glu Lys Ser Arg His
 165 170 175
 cac ctc ccc aca gcc tta gaa aac gcg caa aaa tcc ctt tca tct tct 576
 His Leu Pro Thr Ala Leu Glu Asn Ala Gln Lys Ser Leu Ser Ser Ser
 180 185 190
 tta aat aaa acc atg gaa gca ttg att caa aca aac cct aac caa cga 624
 Leu Asn Lys Thr Met Glu Ala Leu Ile Gln Thr Asn Pro Asn Gln Arg
 195 200 205
 ggg att ttt gaa aaa gcg atc aaa aac gcg gtc att ttg act tca ggg 672
 Gly Ile Phe Glu Lys Ala Ile Lys Asn Gly Val Ile Leu Thr Ser Gly
 210 215 220
 gct tgc ttt agc atg tat aag gat ttc aaa aac caa gct tct tgg gaa 720
 Ala Cys Phe Ser Met Tyr Lys Asp Phe Lys Asn Gln Ala Ser Trp Glu
 225 230 235 240
 agc aaa aaa gaa gag tgt tac aat gca tgg cgg aat tta acc aac gct 768

Ser Lys Lys Glu Glu Cys Tyr Asn Ala Trp Arg Asn Leu Thr Asn Ala
 245 250 255
 tac ccc ctg acg ctt tta aca gcg ttg ata aat ctg aag aaa gct tat 816
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 260 265 270
 tat tct 822
 Tyr Ser
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 His Asp Gln Tyr Glu Arg Met Lys Lys Ser Gly Ser Leu Asn Thr Glu
 35 40 45
 Asn Leu Asp Ser His Ile Gln Ala Asn Ser Leu Gln Glu Leu Asn Gln
 50 55 60
 Lys Leu Leu Gln Phe Val Gly Ala Asp Arg Lys Tyr Met Pro Tyr Thr
 65 70 75 80
 Lys Ala Val Gln Ile Ser Leu Asn Asn Pro Asn Leu Lys Asp Leu Glu
 85 90 95
 Val Ile Asp Thr Pro Gly Val Asn Asp Pro Ile Ala Ser Arg Glu Glu
 100 105 110
 Arg Thr Lys Ala Leu Leu Lys Asp Cys Asp Val Val Phe Ile Ile Ser
 115 120 125
 Ser Ser Asn Gln Phe Leu Thr Glu Ser Asp Met Ser Leu Phe Asp Arg
 130 135 140
 Val Ser Asn Lys Glu Ser Leu Gln Glu Ile Tyr Phe Val Ala Ser Gln
 145 150 155 160
 Ala Asp Ser Ala Val Leu Ser Met Ser Glu Val Glu Lys Ser Arg His
 165 170 175
 His Leu Pro Thr Ala Leu Glu Asn Ala Gln Lys Ser Leu Ser Ser Ser
 180 185 190
 Leu Asn Lys Thr Met Glu Ala Leu Ile Gln Thr Asn Pro Asn Gln Arg
 195 200 205
 Gly Ile Phe Glu Lys Ala Ile Lys Asn Gly Val Ile Leu Thr Ser Gly
 210 215 220
 Ala Cys Phe Ser Met Tyr Lys Asp Phe Lys Asn Gln Ala Ser Trp Glu
 225 230 235 240
 Ser Lys Lys Glu Glu Cys Tyr Asn Ala Trp Arg Asn Leu Thr Asn Ala
 245 250 255
 Tyr Pro Leu Thr Leu Leu Thr Ala Leu Ile Asn Leu Lys Lys Ala Tyr
 260 265 270
 Tyr Ser
 <210> 103
 <211> 711
 <212> DNA
 <213> Helicobacter pylori
 <220>
 <221> CDS
 <222> (1)..(711)
 <400> 103
 agc gaa aaa aat ata gaa aag gtt ttg aac gcc tat gat aag caa caa 48
 Ser Glu Lys Asn Ile Glu Lys Val Leu Asn Ala Tyr Asp Lys Gln Gln
 1 5 10 15
 cac cac cat caa gac gat ctc gct att cag tat tta cca gcc gtg cgc 96
 His His His Gln Asp Asp Leu Ala Ile Gln Tyr Leu Pro Ala Val Arg
 20 25 30

gcc atg gcg ttt cgt cta aaa gag cgc ttg ccc agc tct att gat ttt 144
 Ala Met Ala Phe Arg Leu Lys Glu Arg Leu Pro Ser Ser Ile Asp Phe
 35 40 45
 aac gat ctg gtt tct att ggc act gaa gaa ttg att aaa tta gcc agg 192
 Asn Asp Leu Val Ser Ile Gly Thr Glu Glu Leu Ile Lys Leu Ala Arg
 50 55 60
 cgt tat gag agc gcg tta aac gat tct ttt tgg ggg tat gcg aag act 240
 Arg Tyr Glu Ser Ala Leu Asn Asp Ser Phe Trp Gly Tyr Ala Lys Thr
 65 70 75 80
 cgt gtc aat ggg gcg atg tta gat tat ttg cgc tct tta gat gtg att 288
 Arg Val Asn Gly Ala Met Leu Asp Tyr Leu Arg Ser Leu Asp Val Ile
 85 90 95
 tct cgc tct agc agg aaa ctc att aaa agc att gat att gaa atc acc 336
 Ser Arg Ser Ser Arg Lys Leu Ile Lys Ser Ile Asp Ile Glu Ile Thr
 100 105 110
 aaa cac ctt aat gag cat ggg aaa gag cct agc gat gcg tat tta gcg 384
 Lys His Leu Asn Glu His Gly Lys Glu Pro Ser Asp Ala Tyr Leu Ala
 115 120 125
 caa act tta ggc gaa aat att gaa aaa att aaa gaa gcc aaa acg gct 432
 Gln Thr Leu Gly Glu Asn Ile Glu Lys Ile Lys Glu Ala Lys Thr Ala
 130 135 140
 tca gat att tat gcg tta gtg cca ata gat gaa caa ttc aat gcg att 480
 Ser Asp Ile Tyr Ala Leu Val Pro Ile Asp Glu Gln Phe Asn Ala Ile
 145 150 155 160
 gag caa gat gaa atc act aaa aaa att gaa gca gaa gag ttg tta gag 528
 Glu Gln Asp Glu Ile Thr Lys Lys Ile Glu Ala Glu Glu Leu Leu Glu
 165 170 175
 cat gtc caa aaa gcg ctg aat caa atg agc gaa aga gag caa atc ctt 576
 His Val Gln Lys Ala Leu Asn Gln Met Ser Glu Arg Glu Gln Ile Leu
 180 185 190
 atc cag ctt tat tac ttt gaa gag ttg aat ttg agc gag att aaa gag 624
 Ile Gln Leu Tyr Tyr Phe Glu Glu Leu Asn Leu Ser Glu Ile Lys Glu
 195 200 205
 att tta ggc att act gaa tgc cgc att tct caa atc att aaa gaa gtg 672
 Ile Leu Gly Ile Thr Glu Ser Arg Ile Ser Gln Ile Ile Lys Glu Val
 210 215 220
 att aaa aag gtg cgt aaa tcc tta gga gtg gat cat ggc 711
 Ile Lys Lys Val Arg Lys Ser Leu Gly Val Asp His Gly
 225 230 235
 <210> 104
 <211> 237
 <212> PRT
 <213> *Helicobacter pylori*
 <400> 104
 Ser Glu Lys Asn Ile Glu Lys Val Leu Asn Ala Tyr Asp Lys Gln Gln
 1 5 10 15
 His His His Gln Asp Asp Leu Ala Ile Gln Tyr Leu Pro Ala Val Arg
 20 25 30
 Ala Met Ala Phe Arg Leu Lys Glu Arg Leu Pro Ser Ser Ile Asp Phe
 35 40 45
 Asn Asp Leu Val Ser Ile Gly Thr Glu Glu Leu Ile Lys Leu Ala Arg
 50 55 60
 Arg Tyr Glu Ser Ala Leu Asn Asp Ser Phe Trp Gly Tyr Ala Lys Thr
 65 70 75 80
 Arg Val Asn Gly Ala Met Leu Asp Tyr Leu Arg Ser Leu Asp Val Ile
 85 90 95
 Ser Arg Ser Ser Arg Lys Leu Ile Lys Ser Ile Asp Ile Glu Ile Thr
 100 105 110
 Lys His Leu Asn Glu His Gly Lys Glu Pro Ser Asp Ala Tyr Leu Ala
 115 120 125
 Gln Thr Leu Gly Glu Asn Ile Glu Lys Ile Lys Glu Ala Lys Thr Ala

130 135 140
 Ser Asp Ile Tyr Ala Leu Val Pro Ile Asp Glu Gln Phe Asn Ala Ile
 145 150 155 160
 Glu Gln Asp Glu Ile Thr Lys Lys Ile Glu Ala Glu Glu Leu Leu Glu
 165 170 175
 His Val Gln Lys Ala Leu Asn Gln Met Ser Glu Arg Glu Gln Ile Leu
 180 185 190
 Ile Gln Leu Tyr Tyr Phe Glu Glu Leu Asn Leu Ser Glu Ile Lys Glu
 195 200 205
 Ile Leu Gly Ile Thr Glu Ser Arg Ile Ser Gln Ile Ile Lys Glu Val
 210 215 220
 Ile Lys Lys Val Arg Lys Ser Leu Gly Val Asp His Gly
 225 230 235
 <210> 105
 <211> 1134
 <212> DNA
 <213> *Helicobacter pylori*
 <220>
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 <222> (1)..(1134)
 <400> 105
 gaa tac aac cgc ctc aaa caa cgc acc gag cat gat tta gaa atg att 48
 Glu Tyr Asn Arg Leu Lys Gln Arg Thr 10 His Asp Leu Glu Met Ile 15
 1 5
 agc gcg acc ggt gtg tgt aag ggc att gaa aat tac gcg cgc cat ttc 96
 Ser Ala Thr Gly Val Cys Lys Gly Ile Glu Asn Tyr Ala Arg His Phe 20 25 30
 acc ggt aaa gcc cct aac gaa acg cct ttt tgc ttg ttt gat tat tta 144
 Thr Gly Lys Ala Pro Asn Glu Thr Pro Phe Cys Leu Phe Asp Tyr Leu 35 40 45
 ggg att ttt gag cgg gag ttt tta gtc att gtg gat gaa agc cat gtg 192
 Gly Ile Phe Glu Arg Glu Phe Leu Val Ile Val Asp Glu Ser His Val 50 55 60
 agt ttg cca cag ttt ggg ggg atg tat gca ggg gat atg agc agg aaa 240
 Ser Leu Pro Gln Phe Gly Gly Met Tyr Ala Gly Asp Met Ser Arg Lys 65 70 75 80
 agt gtt tta gtg gaa tat ggt ttt aga ttg cct agc gct tta gac aac 288
 Ser Val Leu Val Glu Tyr Gly Phe Arg Leu Pro Ser Ala Leu Asp Asn 85 90 95
 cgc cct tta aaa ttt gat gaa ttt atc cat aaa aat tgc cag ttc ctt 336
 Arg Pro Leu Lys Phe Asp Glu Phe Ile His Lys Asn Cys Gln Phe Leu 100 105 110
 ttt gtg tcc gct acg ccc aat aag cta gaa tta gag ctt tcc aaa aag 384
 Phe Val Ser Ala Thr Pro Asn Lys Leu Glu Leu Glu Ser Lys Lys 115 120 125
 aat gtc gct gag caa atc att cgc cct aca ggg ctt tta gac cct aaa 432
 Asn Val Ala Glu Gln Ile Ile Arg Pro Thr Gly Leu Leu Asp Pro Lys 130 135 140
 ttt gaa gtg cga gac agc gat aag caa gtc cag gat ttg ttt gat gaa 480
 Phe Glu Val Arg Asp Ser Asp Lys Gln Val Gln Asp Leu Phe Asp Glu 145 150 155 160
 atc aag tta gtg gtg gct aga ggt gaa agg gtg ctc atc acc acg ctc 528
 Ile Lys Leu Val Ala Arg Gly Glu Arg Val Leu Ile Thr Thr Leu 165 170 175
 act aaa aaa atg gca gaa gaa ttg tgc aaa tat tat gct gaa tgg ggc 576
 Thr Lys Lys Met Ala Glu Glu Leu Cys Lys Tyr Tyr Ala Glu Trp Gly 180 185 190
 ttg aag gcg cgt tac atg cat agt gaa att gat gcg att gaa agg aat 624
 Leu Lys Ala Arg Tyr Met His Ser Glu Ile Asp Ala Ile Glu Arg Asn 195 200 205
 cac atc atc cgc tct tta agg ctt aaa gaa ttt gac att tta ata ggg 672

His Ile Ile Arg Ser Leu Arg Leu Lys Glu Phe Asp Ile Leu Ile Gly
 210 215 220
 atc aat ctt tta aga gaa ggg ctg gat ttg cct gaa gtc tct tta gta 720
 Ile Asn Leu Leu Arg Glu Gly Leu Asp Leu Pro Glu Val Ser Leu Val
 225 230 235 240
 gcg atc atg gat gcg gat aaa gaa ggg ttt tta agg agt gaa aca agc 768
 Ala Ile Met Asp Ala Asp Lys Glu Gly Phe Leu Arg Ser Glu Thr Ser
 245 250 255
 ctc att caa acc atg ggg cga gcc gct aga aac gct aat ggc aag gtt 816
 Leu Ile Gln Thr Met Gly Arg Ala Ala Arg Asn Ala Asn Gly Lys Val
 260 265 270
 tta tta tac gct aaa aag atc act caa agc atg caa aaa gcc ttt gag 864
 Leu Leu Tyr Ala Lys Lys Ile Thr Gln Ser Met Gln Lys Ala Phe Glu
 275 280 285
 atc act agt tac agg cgc gcc aaa caa gaa gag ttc aat aaa atc cat 912
 Ile Thr Ser Tyr Arg Arg Ala Lys Gln Glu Glu Phe Asn Lys Ile His
 290 295 300
 aac atc acc ccc aaa acc gtt acg cgc gct tta gaa gag gaa ttg aaa 960
 Asn Ile Thr Pro Lys Thr Val Thr Arg Ala Leu Glu Glu Glu Leu Lys
 305 310 315 320
 tta aga gac gat gaa att aga atc gct aaa gcc tta aaa aag gac aaa 1008
 Leu Arg Asp Asp Glu Ile Arg Ile Ala Lys Ala Leu Lys Lys Asp Lys
 325 330 335
 atg cct aaa agt gaa agg gaa aaa atc att aaa gaa ttg gat aaa aaa 1056
 Met Pro Lys Ser Glu Arg Glu Lys Ile Ile Lys Glu Leu Asp Lys Lys
 340 345 350
 atg cga gaa tgc acg aag aat ttg gat ttt gaa gaa gcg atg cgt ttg 1104
 Met Arg Glu Cys Thr Lys Asn Leu Asp Phe Glu Glu Ala Met Arg Leu
 355 360 365
 aga gac gaa atc gct caa tta aga acg ctt 1134
 Arg Asp Glu Ile Ala Gln Leu Arg Thr Leu
 370 375
 <210> 106
 <211> 378
 <212> PRT
 <213> *Helicobacter pylori*
 <400> 106
 Glu Tyr Asn Arg Leu Lys Gln Arg Thr Glu His Asp Leu Glu Met Ile
 1 5 10 15
 Ser Ala Thr Gly Val Cys Lys Gly Ile Glu Asn Tyr Ala Arg His Phe
 20 25 30
 Thr Gly Lys Ala Pro Asn Glu Thr Pro Phe Cys Leu Phe Asp Tyr Leu
 35 40 45
 Gly Ile Phe Glu Arg Glu Phe Leu Val Ile Val Asp Glu Ser His Val
 50 55 60
 Ser Leu Pro Gln Phe Gly Gly Met Tyr Ala Gly Asp Met Ser Arg Lys
 65 70 75 80
 Ser Val Leu Val Glu Tyr Gly Phe Arg Leu Pro Ser Ala Leu Asp Asn
 85 90 95
 Arg Pro Leu Lys Phe Asp Glu Phe Ile His Lys Asn Cys Gln Phe Leu
 100 105 110
 Phe Val Ser Ala Thr Pro Asn Lys Leu Glu Leu Glu Leu Ser Lys Lys
 115 120 125
 Asn Val Ala Glu Gln Ile Ile Arg Pro Thr Gly Leu Leu Asp Pro Lys
 130 135 140
 Phe Glu Val Arg Asp Ser Asp Lys Gln Val Gln Asp Leu Phe Asp Glu
 145 150 155 160
 Ile Lys Leu Val Val Ala Arg Gly Glu Arg Val Leu Ile Thr Thr Leu
 165 170 175
 Thr Lys Lys Met Ala Glu Glu Leu Cys Lys Tyr Tyr Ala Glu Trp Gly
 180 185 190

Leu Lys Ala Arg Tyr Met His Ser Glu Ile Asp Ala Ile Glu Arg Asn
 195 200 205
 His Ile Ile Arg Ser Leu Arg Leu Lys Glu Phe Asp Ile Leu Ile Gly
 210 215 220
 Ile Asn Leu Leu Arg Glu Gly Leu Asp Leu Pro Glu Val Ser Leu Val
 225 230 235 240
 Ala Ile Met Asp Ala Asp Lys Glu Gly Phe Leu Arg Ser Glu Thr Ser
 245 250 255
 Leu Ile Gln Thr Met Gly Arg Ala Ala Arg Asn Ala Asn Gly Lys Val
 260 265 270
 Leu Leu Tyr Ala Lys Lys Ile Thr Gln Ser Met Gln Lys Ala Phe Glu
 275 280 285
 Ile Thr Ser Tyr Arg Arg Ala Lys Gln Glu Glu Phe Asn Lys Ile His
 290 295 300
 Asn Ile Thr Pro Lys Thr Val Thr Arg Ala Leu Glu Glu Glu Leu Lys
 305 310 315 320
 Leu Arg Asp Asp Glu Ile Arg Ile Ala Lys Ala Leu Lys Lys Asp Lys
 325 330 335
 Met Pro Lys Ser Glu Arg Glu Lys Ile Ile Lys Glu Leu Asp Lys Lys
 340 345 350
 Met Arg Glu Cys Thr Lys Asn Leu Asp Phe Glu Glu Ala Met Arg Leu
 355 360 365
 Arg Asp Glu Ile Ala Gln Leu Arg Thr Leu
 370 375

<210> 107

<211> 499

<212> DNA

<213> Helicobacter pylori

<220>

<221> CDS

<222> (1)..(498)

<400> 107

gaa tcc tta cga gcc tta aaa gct tgc caa gaa gtg cag gct aac acg 48
 Glu Ser Leu Arg Ala Leu Lys Ala Ser Gln Glu Val Gln Ala Asn Thr
 1 5 10 15
 ctt aag cag caa tgc caa act tta gag gat ttg agg aat gag att cac 96
 Leu Lys Gln Gln Ser Gln Thr Leu Glu Asp Leu Arg Asn Glu Ile His
 20 25 30
 gct aac cag caa gct atc cag cag tta gac aag caa aat aaa gag atg 144
 Ala Asn Gln Gln Ala Ile Gln Gln Leu Asp Lys Gln Asn Lys Glu Met
 35 40 45
 agt gaa tta ttg acc aag tta agc cag gat ttg gtt tca caa atc gcc 192
 Ser Glu Leu Leu Thr Lys Leu Ser Gln Asp Leu Val Ser Gln Ile Ala
 50 55 60
 tta atc caa aaa gct ctc aaa gaa caa gag gaa aaa gct gaa aag ccg 240
 Leu Ile Gln Lys Ala Leu Lys Glu Gln Glu Glu Lys Ala Glu Lys Pro
 65 70 75 80
 ctc aaa tca aac gct ccg gct aat aaa acc ccc tct ttg aaa gcc gaa 288
 Leu Lys Ser Asn Ala Pro Ala Asn Lys Thr Pro Ser Leu Lys Ala Glu
 85 90 95
 tcc cca aaa aat caa gag gga aaa act caa gaa aag gcg aaa att gag 336
 Ser Pro Lys Asn Gln Glu Gly Lys Thr Gln Glu Lys Ala Lys Ile Glu
 100 105 110
 ttt gat aaa gac ttg tct aag caa aaa gag atc ttt caa gaa gct ctg 384
 Phe Asp Lys Asp Leu Ser Lys Gln Lys Glu Ile Phe Gln Glu Ala Leu
 115 120 125
 tct ttt ttt aaa aat aaa tcc tat gca gaa gcc aaa gag cgt ttg ttg 432
 Ser Phe Phe Lys Asn Lys Ser Tyr Ala Glu Ala Lys Glu Arg Leu Leu
 130 135 140
 tgg tta gaa gcc aat agt tac aga ctt tat tat gtg cgt tat gtt ctt 480
 Trp Leu Glu Ala Asn Ser Tyr Arg Leu Tyr Tyr Val Arg Tyr Val Leu

145 150 155 160 499
 gga gaa gtg gct tat ggg g
 Gly Glu Val Ala Tyr Gly
 165
 <210> 108
 <211> 166
 <212> PRT
 <213> *Helicobacter pylori*
 <400> 108
 Glu Ser Leu Arg Ala Leu Lys Ala Ser Gln Glu Val Gln Ala Asn Thr
 1 5 10 15
 Leu Lys Gln Gln Ser Gln Thr Leu Glu Asp Leu Arg Asn Glu Ile His
 20 25 30
 Ala Asn Gln Gln Ala Ile Gln Gln Leu Asp Lys Gln Asn Lys Glu Met
 35 40 45
 Ser Glu Leu Leu Thr Lys Leu Ser Gln Asp Leu Val Ser Gln Ile Ala
 50 55 60
 Leu Ile Gln Lys Ala Leu Lys Glu Gln Glu Lys Ala Glu Lys Pro
 65 70 75 80
 Leu Lys Ser Asn Ala Pro Ala Asn Lys Thr Pro Ser Leu Lys Ala Glu
 85 90 95
 Ser Pro Lys Asn Gln Glu Gly Lys Thr Gln Glu Lys Ala Lys Ile Glu
 100 105 110
 Phe Asp Lys Asp Leu Ser Lys Gln Lys Glu Ile Phe Gln Glu Ala Leu
 115 120 125
 Ser Phe Phe Lys Asn Lys Ser Tyr Ala Glu Ala Lys Glu Arg Leu Leu
 130 135 140
 Trp Leu Glu Ala Asn Ser Tyr Arg Leu Tyr Tyr Val Arg Tyr Val Leu
 145 150 155 160
 Gly Glu Val Ala Tyr Gly
 165
 <210> 109
 <211> 133
 <212> DNA
 <213> *Helicobacter pylori*
 <220>
 <221> CDS
 <222> (1)..(132)
 <400> 109
 cac act cta aaa gaa atg ctc acc att aaa tcc gat gat att aga ggc 48
 His Thr Leu Lys Glu Met Leu Thr Ile Lys Ser Asp Asp Ile Arg Gly
 1 5 10 15
 aga gag aac gct tat agg gct atc gct aaa ggt gag caa gtg ggc gag 96
 Arg Glu Asn Ala Tyr Arg Ala Ile Ala Lys Gly Glu Gln Val Gly Glu
 20 25 30
 agt gaa atc cct gag act ttc tat gtt ttg act aaa g 133
 Ser Glu Ile Pro Glu Thr Phe Tyr Val Leu Thr Lys
 35 40
 <210> 110
 <211> 44
 <212> PRT
 <213> *Helicobacter pylori*
 <400> 110
 His Thr Leu Lys Glu Met Leu Thr Ile Lys Ser Asp Asp Ile Arg Gly
 1 5 10 15
 Arg Glu Asn Ala Tyr Arg Ala Ile Ala Lys Gly Glu Gln Val Gly Glu
 20 25 30
 Ser Glu Ile Pro Glu Thr Phe Tyr Val Leu Thr Lys
 35 40
 <210> 111
 <211> 932

<212> DNA

<213> *Helicobacter pylori*

<220>

<221> CDS

<222> (1)..(930)

<400> 111

tta gcc caa atg cgt tta gcc att gaa gcg gct gaa ggc tct gat ttg	48
Leu Ala Gln Met Arg Leu Ala Ile Glu Ala Glu Gly Ser Asp Leu	
1 5 10 15	
agc aac gct aac atg ctt ttt aaa gaa gct ttt tct aac gcc aaa gac	96
Ser Asn Ala Asn Met Leu Phe Lys Glu Ala Phe Ser Asn Ala Lys Asp	
20 25 30	
aaa gag agt gcg agt gaa atc gcg ctt aat tgg gct gaa gca gag ata	144
Lys Glu Ser Ala Ser Glu Ile Ala Leu Asn Trp Ala Glu Ala Glu Ile	
35 40 45	
aac tat caa aat ttt aat aac gct aaa tac ctc att gat aag gtg gtc	192
Asn Tyr Gln Asn Phe Asn Asn Ala Lys Tyr Leu Ile Asp Lys Val Val	
50 55 60	
caa tcc aac cct gat tat att tct acg cat agc gaa tca gcc cta gac	240
Gln Ser Asn Pro Asp Tyr Ile Ser Thr His Ser Glu Ser Ala Leu Asp	
65 70 75 80	
ttg ctc aag tta ttg aaa aaa aac cag atg aat gca agc gcg att gag	288
Leu Leu Lys Leu Lys Lys Asn Gln Met Asn Ala Ser Ala Ile Glu	
85 90 95	
atc gct cac ttg ctc ctc aat caa gat gat gat ctg aaa gct aaa gag	336
Ile Ala His Leu Leu Leu Asn Gln Asp Asp Asp Leu Lys Ala Lys Glu	
100 105 110	
caa gcg ctt tat gat tta gga gcg ttg tat gca agg atc aag gac ttt	384
Gln Ala Leu Tyr Asp Leu Gly Ala Leu Tyr Ala Arg Ile Lys Asp Phe	
115 120 125	
aaa aac gcc cac ctt tac aat ctg caa tat ttg cag gac cat gcg gaa	432
Lys Asn Ala His Leu Tyr Asn Leu Gln Tyr Leu Gln Asp His Ala Glu	
130 135 140	
ctg gat aaa gct tct gtc gtt agg gcg cgc gat gaa aaa gcc ctt ttt	480
Leu Asp Lys Ala Ser Val Val Arg Ala Arg Asp Glu Lys Ala Leu Phe	
145 150 155 160	
tcc atg gag ggg aac acg caa gaa aaa atc gcc cac tat gac aaa atc	528
Ser Met Glu Gly Asn Thr Gln Glu Lys Ile Ala His Tyr Asp Lys Ile	
165 170 175	
att caa aat ttc cct aat tct aat gaa gcc cta aag gct tta gaa ttg	576
Ile Gln Asn Phe Pro Asn Ser Asn Glu Ala Leu Lys Ala Leu Glu Leu	
180 185 190	
aaa gcc caa cta ttg ttt gaa aac aag cgt tat gct gaa gtg tta agc	624
Lys Ala Gln Leu Leu Phe Glu Asn Lys Arg Tyr Ala Glu Val Leu Ser	
195 200 205	
atg caa aaa aat ttg cct aaa gat tcc cct ttg atc caa aaa acg ctc	672
Met Gln Lys Asn Leu Pro Lys Asp Ser Pro Leu Ile Gln Lys Thr Leu	
210 215 220	
aat gtc ctt gct aaa acc cca tta gag aac cat cgt tgt gaa gaa gcc	720
Asn Val Leu Ala Lys Thr Pro Leu Glu Asn His Arg Cys Glu Glu Ala	
225 230 235 240	
tta aaa tat tta tcc caa atc aca acc ttt gaa ttc agc ccc aaa gaa	768
Leu Lys Tyr Leu Ser Gln Ile Thr Thr Phe Glu Phe Ser Pro Lys Glu	
245 250 255	
gaa atc caa gcc ttt gat tgc ttg tat ttc gca tcg ctc aaa gaa aaa	816
Glu Ile Gln Ala Phe Asp Cys Leu Tyr Phe Ala Ser Leu Lys Glu Lys	
260 265 270	
gcg caa atc att gcc cta aac gct ttt aaa acg gct aaa gcc cct agc	864
Ala Gln Ile Ile Ala Leu Asn Ala Phe Lys Thr Ala Lys Ala Pro Ser	
275 280 285	
gag aaa tta ata tgg ctt tat cgt ttg ggg cgc aat tac tac cgc tta	912

Glu Lys Leu Ile Trp Leu Tyr Arg Leu Gly Arg Asn Tyr Tyr Arg Leu
 290 295 300
 ggg gat ttt aaa aat tcc ac
 Gly Asp Phe Lys Asn Ser
 305 310
 <210> 112
 <211> 310
 <212> PRT
 <213> Helicobacter pylori
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 Leu Ala Gln Met Arg Leu Ala Ile Glu Ala Ala Glu Gly Ser Asp Leu
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 Ser Asn Ala Asn Met Leu Phe Lys Glu Ala Phe Ser Asn Ala Lys Asp
 20 25 30
 Lys Glu Ser Ala Ser Glu Ile Ala Leu Asn Trp Ala Glu Ala Glu Ile
 35 40 45
 Asn Tyr Gln Asn Phe Asn Asn Ala Lys Tyr Leu Ile Asp Lys Val Val
 50 55 60
 Gln Ser Asn Pro Asp Tyr Ile Ser Thr His Ser Glu Ser Ala Leu Asp
 65 70 75 80
 Leu Leu Lys Leu Leu Lys Lys Asn Gln Met Asn Ala Ser Ala Ile Glu
 85 90 95
 Ile Ala His Leu Leu Leu Asn Gln Asp Asp Asp Leu Lys Ala Lys Glu
 100 105 110
 Gln Ala Leu Tyr Asp Leu Gly Ala Leu Tyr Ala Arg Ile Lys Asp Phe
 115 120 125
 Lys Asn Ala His Leu Tyr Asn Leu Gln Tyr Leu Gln Asp His Ala Glu
 130 135 140
 Leu Asp Lys Ala Ser Val Val Arg Ala Arg Asp Glu Lys Ala Leu Phe
 145 150 155 160
 Ser Met Glu Gly Asn Thr Gln Glu Lys Ile Ala His Tyr Asp Lys Ile
 165 170 175
 Ile Gln Asn Phe Pro Asn Ser Asn Glu Ala Leu Lys Ala Leu Glu Leu
 180 185 190
 Lys Ala Gln Leu Leu Phe Glu Asn Lys Arg Tyr Ala Glu Val Leu Ser
 195 200 205
 Met Gln Lys Asn Leu Pro Lys Asp Ser Pro Leu Ile Gln Lys Thr Leu
 210 215 220
 Asn Val Leu Ala Lys Thr Pro Leu Glu Asn His Arg Cys Glu Glu Ala
 225 230 235 240
 Leu Lys Tyr Leu Ser Gln Ile Thr Thr Phe Glu Phe Ser Pro Lys Glu
 245 250 255
 Glu Ile Gln Ala Phe Asp Cys Leu Tyr Phe Ala Ser Leu Lys Glu Lys
 260 265 270
 Ala Gln Ile Ile Ala Leu Asn Ala Phe Lys Thr Ala Lys Ala Pro Ser
 275 280 285
 Glu Lys Leu Ile Trp Leu Tyr Arg Leu Gly Arg Asn Tyr Tyr Arg Leu
 290 295 300
 Gly Asp Phe Lys Asn Ser
 305 310
 <210> 113
 <211> 591
 <212> DNA
 <213> Helicobacter pylori
 <220>
 <221> CDS
 <222> (1)..(591)
 <400> 113
 gcg aac aaa aag aaa aaa aaa gac gaa tac aac aaa ccg gcg atc ttt
 Ala Asn Lys Lys Lys Lys Lys Asp Glu Tyr Asn Lys Pro Ala Ile Phe
 1 5 10 15

932

48

tgg tat caa ggg att ttg aga gaa atc ctt ttt gct aat tta gaa aca 96
 Trp Tyr Gln Gly Ile Leu Arg Glu Ile Leu Phe Ala Asn Leu Glu Thr
 20 25 30
 gcg gac aat tac tat tct tct tta caa agc gaa cac atc aat tcc ccc 144
 Ala Asp Asn Tyr Tyr Ser Ser Leu Gln Ser Glu His Ile Asn Ser Pro
 35 40 45
 ctt gtc cca gaa gcg atg cta gct tta ggg caa gcg cac atg aaa aag 192
 Leu Val Pro Glu Ala Met Leu Ala Leu Gly Gln Ala His Met Lys Lys
 50 55 60
 aaa gag tat gtt tta gcg tct ttt tac ttt gat gaa tac atc aag cgc 240
 Lys Glu Tyr Val Leu Ala Ser Phe Tyr Phe Asp Glu Tyr Ile Lys Arg
 65 70 75 80
 ttt ggg act aag gac aat gtg gat tat ttg act ttt tta aaa ttg caa 288
 Phe Gly Thr Lys Asp Asn Val Asp Tyr Leu Thr Phe Leu Lys Leu Gln
 85 90 95
 tcg cat tat tac gct ttc aaa aac cat tct aaa gac cag gaa ttt atc 336
 Ser His Tyr Tyr Ala Phe Lys Asn His Ser Lys Asp Gln Glu Phe Ile
 100 105 110
 tct aat tct att gtg agt tta ggc gaa ttt ata gaa aaa tac cct aac 384
 Ser Asn Ser Ile Val Ser Leu Gly Glu Phe Ile Glu Lys Tyr Pro Asn
 115 120 125
 agc cgt tac cgc ccc tat gta gaa tac atg caa atc aaa ttc att tta 432
 Ser Arg Tyr Arg Pro Tyr Val Glu Tyr Met Gln Ile Lys Phe Ile Leu
 130 135 140
 ggg caa aat gag ctc aat cgc gcg atc gcg aat gtc tat aaa aaa cgc 480
 Gly Gln Asn Glu Leu Asn Arg Ala Ile Ala Asn Val Tyr Lys Lys Arg
 145 150 155 160
 cac aag cct gag ggc gtg aaa cgc tat tta gaa agg ata gat gag act 528
 His Lys Pro Glu Gly Val Lys Arg Tyr Leu Glu Arg Ile Asp Glu Thr
 165 170 175
 tta gaa aaa gag act aaa ccc aaa cca tcg cac atg cct tgg tat gtg 576
 Leu Glu Lys Glu Thr Lys Pro Lys Pro Ser His Met Pro Trp Tyr Val
 180 185 190
 tta att ttt gat tgg 591
 Leu Ile Phe Asp Trp
 195

<210> 114

<211> 197

<212> PRT

<213> Helicobacter pylori

<400> 114

Ala Asn Lys Lys Lys Lys Lys Asp Glu Tyr Asn Lys Pro Ala Ile Phe
 1 5 10 15
 Trp Tyr Gln Gly Ile Leu Arg Glu Ile Leu Phe Ala Asn Leu Glu Thr
 20 25 30
 Ala Asp Asn Tyr Tyr Ser Ser Leu Gln Ser Glu His Ile Asn Ser Pro
 35 40 45
 Leu Val Pro Glu Ala Met Leu Ala Leu Gly Gln Ala His Met Lys Lys
 50 55 60
 Lys Glu Tyr Val Leu Ala Ser Phe Tyr Phe Asp Glu Tyr Ile Lys Arg
 65 70 75 80
 Phe Gly Thr Lys Asp Asn Val Asp Tyr Leu Thr Phe Leu Lys Leu Gln
 85 90 95
 Ser His Tyr Tyr Ala Phe Lys Asn His Ser Lys Asp Gln Glu Phe Ile
 100 105 110
 Ser Asn Ser Ile Val Ser Leu Gly Glu Phe Ile Glu Lys Tyr Pro Asn
 115 120 125
 Ser Arg Tyr Arg Pro Tyr Val Glu Tyr Met Gln Ile Lys Phe Ile Leu
 130 135 140
 Gly Gln Asn Glu Leu Asn Arg Ala Ile Ala Asn Val Tyr Lys Lys Arg
 145 150 155 160

His	Lys	Pro	Glu	Gly	Val	Lys	Arg	Tyr	Leu	Glu	Arg	Ile	Asp	Glu	Thr		
				165					170					175			
Leu	Glu	Lys	Glu	Thr	Lys	Pro	Lys	Pro	Ser	His	Met	Pro	Trp	Tyr	Val		
			180					185					190				
Leu	Ile	Phe	Asp	Trp													
			195														
<210> 115																	
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<212> DNA																	
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<400> 115																	
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Phe	Lys	Pro	Phe	Lys	Asp	Ala	Phe	Tyr	Arg	Asp	Phe	Asn	His	Asn	Glu		
1				5					10					15			
caa	aag	tta	ctg	ata	ggg	gca	gct	aaa	agc	ggg	tgc	att	caa	tct	agc	96	
Gln	Lys	Leu	Leu	Ile	Gly	Ala	Ala	Lys	Ser	Gly	Cys	Ile	Gln	Ser	Ser		
			20					25					30				
gct	gat	aaa	ctg	gct	cag	tta	aaa	acg	cgc	tta	ctc	tac	tgg	caa	gac	144	
Ala	Asp	Lys	Leu	Ala	Gln	Leu	Lys	Thr	Arg	Leu	Leu	Tyr	Trp	Gln	Asp		
			35					40				45					
aaa	tct	ggt	aaa	gtg	gat	tgg	gat	aaa	ccc	att	tta	atc	aag	gac	ttc	192	
Lys	Ser	Val	Lys	Val	Asp	Trp	Asp	Lys	Pro	Ile	Leu	Ile	Lys	Asp	Phe		
	50					55					60						
ttt	aaa	ggc	aat	aat	tac	ctt	tat	agg	agg	ttt	tgt	ttt	tta	ttg	ggg	240	
Phe	Lys	Gly	Asn	Asn	Tyr	Leu	Tyr	Arg	Arg	Phe	Cys	Phe	Leu	Leu	Gly		
	65				70					75					80		
aag	cat	ttt	atg	gac	aga	ttt	tta	aag	aat	aac	gct	aag	gcg	agc	gtg	288	
Lys	His	Phe	Met	Asp	Arg	Phe	Leu	Lys	Asn	Asn	Ala	Lys	Ala	Ser	Val		
				85					90					95			
aaa	gac	ttt	atg	tct	agt	aag	gag	ttt	gtc	gct	aaa	tac	cga	tac	acc	336	
Lys	Asp	Phe	Met	Ser	Ser	Lys	Glu	Phe	Val	Ala	Lys	Tyr	Arg	Tyr	Thr		
			100					105					110				
ccc	aag	caa	aat	aca	gaa	aga	gcg	aaa	aag	ctg	caa	tcg	tat	tta	gag	384	
Pro	Lys	Gln	Asn	Thr	Glu	Arg	Ala	Lys	Lys	Leu	Gln	Ser	Tyr	Leu	Glu		
			115				120					125					
aat	aag	cgc	gat	ttt	ata	ggg	ttt	ggt	caa	gcg	ctt	aac	tct	tta	aaa	432	
Asn	Lys	Arg	Asp	Phe	Ile	Gly	Phe	Val	Gln	Ala	Leu	Asn	Ser	Leu	Lys		
			130			135				140							
gac	aac	ccg	caa	gat	cct	ttt	tta	ccc	aat	gaa	gaa	acg	agc	ttt	ttg	480	
Asp	Asn	Pro	Gln	Asp	Pro	Phe	Leu	Pro	Asn	Glu	Glu	Thr	Ser	Phe	Leu		
	145				150					155							

[illegible]

<210> 117

<211> 399

<212> DNA

<213> *Helicobacter pylori*

<220>

<221> CDS

<222> (1) .. (399)

<400> 117

[illegible]

<210> 118

<211> 133

<212> PRT

<213> *Helicobacter pylori*

<400> 118

Leu	Ala	Leu	Asn	Glu	Leu	Asn	Pro	Gly	Glu	Trp	Val	Val	His	Asp	Asp
1				5					10					15	
Tyr	Gly	Val	Gly	Val	Phe	Ser	Gln	Leu	Val	Gln	His	Ser	Val	Leu	Gly
			20					25					30		
Ser	Lys	Arg	Asp	Phe	Leu	Glu	Ile	Ala	Tyr	Leu	Gly	Glu	Asp	Lys	Leu
		35					40					45			
Leu	Leu	Pro	Val	Glu	Asn	Leu	His	Leu	Ile	Ala	Arg	Tyr	Val	Ala	Gln
	50					55					60				

Ser Asp Ser Val Pro Ala Lys Asp Arg Leu Gly Lys Gly Ser Phe Leu
 65 70 75 80
 Lys Leu Lys Ala Lys Val Arg Thr Lys Leu Leu Glu Ile Ala Ser Lys
 85 90 95
 Ile Ile Glu Leu Ala Ala Glu Arg Asn Leu Ile Leu Gly Lys Lys Met
 100 105 110
 Asp Val His Leu Ala Glu Leu Glu Val Phe Lys Ser His Ala Gly Phe
 115 120 125
 Glu Tyr Thr Ser Asp
 130

<210> 119

<211> 426

<212> DNA

<213> Helicobacter pylori

<220>

<221> CDS

<222> (1)..(426)

<400> 119

ggt tta aac gca ccc atc act tta gaa gac att caa gaa tta agc tcc 48
 Val Leu Asn Ala Pro Ile Thr Leu Glu Asp Ile Gln Glu Leu Ser Ser
 1 5 10 15
 aat gcg ggg gat atg gat ttg caa aag ctc att tta ggg ctt ttt tta 96
 Asn Ala Gly Asp Met Asp Leu Gln Lys Leu Ile Leu Gly Leu Phe Leu
 20 25 30
 aaa aaa agt gcg ctt gat att tat gat tat ttg tta aaa gag ggc aaa 144
 Lys Lys Ser Ala Leu Asp Ile Tyr Asp Tyr Leu Leu Lys Glu Gly Lys
 35 40 45
 aaa gat gcg gat att tta agg ggg tta gag cgc tat ttt tac caa ctt 192
 Lys Asp Ala Asp Ile Leu Arg Gly Leu Glu Arg Tyr Phe Tyr Gln Leu
 50 55 60
 ttt tta ttt ttc gct cat att aaa acg acc ggt tta atg gac gct aaa 240
 Phe Leu Phe Phe Ala His Ile Lys Thr Thr Gly Leu Met Asp Ala Lys
 65 70 75 80
 gag gtt tta ggc tac gct ccc cct aaa gaa att gcc gaa aat tac gct 288
 Glu Val Leu Gly Tyr Ala Pro Pro Lys Glu Ile Ala Glu Asn Tyr Ala
 85 90 95
 aaa aac gcc ttg cgt ttg aaa gaa gcc ggc tat aag agg gtt ttt gaa 336
 Lys Asn Ala Leu Arg Leu Lys Glu Ala Gly Tyr Lys Arg Val Phe Glu
 100 105 110
 att ttt agg tta tgg cac att caa agc atg caa ggg caa aag gaa ttg 384
 Ile Phe Arg Leu Trp His Ile Gln Ser Met Gln Gly Gln Lys Glu Leu
 115 120 125
 ggc ttt ttg tat ttg acc tcc att caa aaa atc att aac ccc 426
 Gly Phe Leu Tyr Leu Thr Ser Ile Gln Lys Ile Ile Asn Pro
 130 135 140

<210> 120

<211> 142

<212> PRT

<213> Helicobacter pylori

<400> 120

Val Leu Asn Ala Pro Ile Thr Leu Glu Asp Ile Gln Glu Leu Ser Ser
 1 5 10 15
 Asn Ala Gly Asp Met Asp Leu Gln Lys Leu Ile Leu Gly Leu Phe Leu
 20 25 30
 Lys Lys Ser Ala Leu Asp Ile Tyr Asp Tyr Leu Leu Lys Glu Gly Lys
 35 40 45
 Lys Asp Ala Asp Ile Leu Arg Gly Leu Glu Arg Tyr Phe Tyr Gln Leu
 50 55 60
 Phe Leu Phe Phe Ala His Ile Lys Thr Thr Gly Leu Met Asp Ala Lys
 65 70 75 80
 Glu Val Leu Gly Tyr Ala Pro Pro Lys Glu Ile Ala Glu Asn Tyr Ala

85 90 95
 Lys Asn Ala Leu Arg Leu Lys Glu Ala Gly Tyr Lys Arg Val Phe Glu
 100 105 110
 Ile Phe Arg Leu Trp His Ile Gln Ser Met Gln Gly Gln Lys Glu Leu
 115 120 125
 Gly Phe Leu Tyr Leu Thr Ser Ile Gln Lys Ile Ile Asn Pro
 130 135 140
 <210> 121
 <211> 297
 <212> DNA
 <213> *Helicobacter pylori*
 <220>
 <221> CDS
 <222> (1)..(297)
 <400> 121
 gaa gaa tgc ggc acg ctt tta gaa ttg agg gaa aaa att tcg ttg ttt 48
 Glu Glu Cys Gly Thr Leu Leu Glu Leu Arg Glu Lys Ile Ser Leu Phe
 1 5 10 15
 tta gag cca aag gat att gtt aaa act tat gaa aat gaa gat ttt aaa 96
 Leu Glu Pro Lys Asp Ile Val Lys Thr Tyr Glu Asn Glu Asp Phe Lys
 20 25 30
 gag cgt tgt tta gcg ctt ttt aac gct cta aca agc atg gat ttt caa 144
 Glu Arg Cys Leu Ala Leu Phe Asn Ala Leu Thr Ser Met Asp Phe Gln
 35 40 45
 gcg tat aag gat ttt gaa agt ttt aaa aaa gaa gcc atg cga tta agc 192
 Ala Tyr Lys Asp Phe Glu Ser Phe Lys Lys Glu Ala Met Arg Leu Ser
 50 55 60
 cag ctt aag ggt aag gat ttt ttc aaa cct ttg cgc atc ctt tta acc 240
 Gln Leu Lys Gly Lys Asp Phe Phe Lys Pro Leu Arg Ile Leu Leu Thr
 65 70 75 80
 ggg aac tcg cat ggc gtt gaa ttg cct ttg att ttc ccc tat atc caa 288
 Gly Asn Ser His Gly Val Glu Leu Pro Leu Ile Phe Pro Tyr Ile Gln
 85 90 95
 agc cat cat 297
 Ser His His
 <210> 122
 <211> 99
 <212> PRT
 <213> *Helicobacter pylori*
 <400> 122
 Glu Glu Cys Gly Thr Leu Leu Glu Leu Arg Glu Lys Ile Ser Leu Phe
 1 5 10 15
 Leu Glu Pro Lys Asp Ile Val Lys Thr Tyr Glu Asn Glu Asp Phe Lys
 20 25 30
 Glu Arg Cys Leu Ala Leu Phe Asn Ala Leu Thr Ser Met Asp Phe Gln
 35 40 45
 Ala Tyr Lys Asp Phe Glu Ser Phe Lys Lys Glu Ala Met Arg Leu Ser
 50 55 60
 Gln Leu Lys Gly Lys Asp Phe Phe Lys Pro Leu Arg Ile Leu Leu Thr
 65 70 75 80
 Gly Asn Ser His Gly Val Glu Leu Pro Leu Ile Phe Pro Tyr Ile Gln
 85 90 95
 Ser His His
 <210> 123
 <211> 42
 <212> DNA
 <213> *Helicobacter pylori*
 <220>
 <221> CDS
 <222> (1)..(42)
 <400> 123

ccc caa atc gta gct aaa gat ttt tta gaa aga tta ggg tta 42
 Pro Gln Ile Val Ala Lys Asp Phe Leu Glu Arg Leu Gly Leu
 1 5 10
 <210> 124
 <211> 14
 <212> PRT
 <213> *Helicobacter pylori*
 <400> 124
 Pro Gln Ile Val Ala Lys Asp Phe Leu Glu Arg Leu Gly Leu
 1 5 10
 <210> 125
 <211> 84
 <212> DNA
 <213> *Helicobacter pylori*
 <220>
 <221> CDS
 <222> (1)..(84)
 <400> 125
 aag aaa gcg att gaa aat aac cag tat aaa atc aac ttg cat gag act 48
 Lys Lys Ala Ile Glu Asn Asn Gln Tyr Lys Ile Asn Leu His Glu Thr
 1 5 10 15
 tct cac aaa atg gca aag gat tta ttg ggg ata agc 84
 Ser His Lys Met Ala Lys Asp Leu Leu Gly Ile Ser
 20 25
 <210> 126
 <211> 28
 <212> PRT
 <213> *Helicobacter pylori*
 <400> 126
 Lys Lys Ala Ile Glu Asn Asn Gln Tyr Lys Ile Asn Leu His Glu Thr
 1 5 10 15
 Ser His Lys Met Ala Lys Asp Leu Leu Gly Ile Ser
 20 25
 <210> 127
 <211> 356
 <212> DNA
 <213> *Helicobacter pylori*
 <220>
 <221> CDS
 <222> (1)..(354)
 <400> 127
 cac att tat gaa aaa gaa gtg gat gct agg gag ctt aag cat ggt gtg 48
 His Ile Tyr Glu Lys Glu Val Asp Ala Arg Glu Leu Lys His Gly Val
 1 5 10 15
 gaa gaa ttt acc gct gat att cct gat gtg aaa gaa gaa gcg ctc gct 96
 Glu Glu Phe Thr Ala Asp Ile Pro Asp Val Lys Glu Glu Ala Leu Ala
 20 25 30
 cat ctt gat gaa agc ggg atc gtt aaa gtc ggt act tat gtg agc gct 144
 His Leu Asp Glu Ser Gly Ile Val Lys Val Gly Thr Tyr Val Ser Ala
 35 40 45
 ggc atg att ttg gtg ggc aaa act tct cct aaa ggc gag att aaa agc 192
 Gly Met Ile Leu Val Gly Lys Thr Ser Pro Lys Gly Glu Ile Lys Ser
 50 55 60
 acg cct gaa gag cgg ctt tta agg gct att ttt ggg gat aaa gcc ggg 240
 Thr Pro Glu Glu Arg Leu Leu Arg Ala Ile Phe Gly Asp Lys Ala Gly
 65 70 75 80
 cat gtg gtc aat aag agt ttg tat tgc cct ccc agt ttg gaa ggc acg 288
 His Val Val Asn Lys Ser Leu Tyr Cys Pro Pro Ser Leu Glu Gly Thr
 85 90 95
 gtg att gat gtg aaa gtc ttc act aaa aaa ggc tat gag aaa gac gcg 336
 Val Ile Asp Val Lys Val Phe Thr Lys Lys Gly Tyr Glu Lys Asp Ala

100 105 110 356
 cga gtt ttg agc gcg tat ga
 Arg Val Leu Ser Ala Tyr
 115
 <210> 128
 <211> 118
 <212> PRT
 <213> Helicobacter pylori
 <400> 128
 His Ile Tyr Glu Lys Glu Val Asp Ala Arg Glu Leu Lys His Gly Val
 1 5 10 15
 Glu Glu Phe Thr Ala Asp Ile Pro Asp Val Lys Glu Glu Ala Leu Ala
 20 25 30
 His Leu Asp Glu Ser Gly Ile Val Lys Val Gly Thr Tyr Val Ser Ala
 35 40 45
 Gly Met Ile Leu Val Gly Lys Thr Ser Pro Lys Gly Glu Ile Lys Ser
 50 55 60
 Thr Pro Glu Glu Arg Leu Leu Arg Ala Ile Phe Gly Asp Lys Ala Gly
 65 70 75 80
 His Val Val Asn Lys Ser Leu Tyr Cys Pro Pro Ser Leu Glu Gly Thr
 85 90 95
 Val Ile Asp Val Lys Val Phe Thr Lys Lys Gly Tyr Glu Lys Asp Ala
 100 105 110
 Arg Val Leu Ser Ala Tyr
 115
 <210> 129
 <211> 698
 <212> DNA
 <213> Helicobacter pylori
 <220>
 <221> CDS
 <222> (1)..(696)
 <400> 129
 tat aag ccc tac acc cca agc aga cgc ttc atg tcg gtg ttg gac tct 48
 Tyr Lys Pro Tyr Thr Pro Ser Arg Arg Phe Met Ser Val Leu Asp Ser
 1 5 10 15
 aaa gac att acc gca aaa agc agt gtc aaa ggc tta ctc act aag ctt 96
 Lys Asp Ile Thr Ala Lys Ser Ser Val Lys Gly Leu Leu Thr Lys Leu
 20 25 30
 aaa gca aca gca ggg aga aac aat aac ggg cgc atc acc agc cgc cac 144
 Lys Ala Thr Ala Gly Arg Asn Asn Asn Gly Arg Ile Thr Ser Arg His
 35 40 45
 aaa gag aga ggg gct aaa aaa ctc tat cgc att att gat ttc aag cgc 192
 Lys Glu Arg Gly Ala Lys Lys Leu Tyr Arg Ile Ile Asp Phe Lys Arg
 50 55 60
 aat aaa tac aat att gaa ggg aaa gtg gct gcg att gag tat gat cct 240
 Asn Lys Tyr Asn Ile Glu Gly Lys Val Ala Ala Ile Glu Tyr Asp Pro
 65 70 75 80
 tac aga aat gcg cgc atc gct ctt gta gtc tat cct gat ggg gac aaa 288
 Tyr Arg Asn Ala Arg Ile Ala Leu Val Val Tyr Pro Asp Gly Asp Lys
 85 90 95
 cgc tat att tta cag cca agc ggt ttg aaa gtg ggc gat agc gtt atc 336
 Arg Tyr Ile Leu Gln Pro Ser Gly Leu Lys Val Gly Asp Ser Val Ile
 100 105 110
 gct gct gaa ggc ggt ttg gat att aaa gtg ggc ttt gcg atg aag tta 384
 Ala Ala Glu Gly Gly Leu Asp Ile Lys Val Gly Phe Ala Met Lys Leu
 115 120 125
 aaa aat atc ccc ata gga acg gtg gtg cat aat att gaa atg cat cca 432
 Lys Asn Ile Pro Ile Gly Thr Val Val His Asn Ile Glu Met His Pro
 130 135 140
 ggg gct ggc ggg caa tta gcc aga agc gca gga atg agc gct caa atc 480

Gly Ala Gly Gly Gln Leu Ala Arg Ser Ala Gly Met Ser Ala Gln Ile
 145 150 155 160
 atg ggt aga gaa aat aaa tac acc att att agg atg cca agc tct gaa 528
 Met Gly Arg Glu Asn Lys Tyr Thr Ile Ile Arg Met Pro Ser Ser Glu
 165 170 175
 atg cgc tac att cta agc gaa tgt atg gcg agt gtt ggc gtg gta ggg 576
 Met Arg Tyr Ile Leu Ser Glu Cys Met Ala Ser Val Gly Val Val Gly
 180 185 190
 aat gag gat ttt atc aat gtc tct atc ggt aag gca ggg cgt aac cgc 624
 Asn Glu Asp Phe Ile Asn Val Ser Ile Gly Lys Ala Gly Arg Asn Arg
 195 200 205
 cac aga ggg atc cgc cca caa act cgt ggt agc gcg atg aac cca gtg 672
 His Arg Gly Ile Arg Pro Gln Thr Arg Gly Ser Ala Met Asn Pro Val
 210 215 220
 gat cac ccg cat ggt ggg ggt gag gg 698
 Asp His Pro His Gly Gly Glu
 225 230

<210> 130

<211> 232

<212> PRT

<213> Helicobacter pylori

<400> 130

Tyr Lys Pro Tyr Thr Pro Ser Arg Arg Phe Met Ser Val Leu Asp Ser
 1 5 10 15
 Lys Asp Ile Thr Ala Lys Ser Ser Val Lys Gly Leu Leu Thr Lys Leu
 20 25 30
 Lys Ala Thr Ala Gly Arg Asn Asn Asn Gly Arg Ile Thr Ser Arg His
 35 40 45
 Lys Glu Arg Gly Ala Lys Lys Leu Tyr Arg Ile Ile Asp Phe Lys Arg
 50 55 60
 Asn Lys Tyr Asn Ile Glu Gly Lys Val Ala Ala Ile Glu Tyr Asp Pro
 65 70 75 80
 Tyr Arg Asn Ala Arg Ile Ala Leu Val Val Tyr Pro Asp Gly Asp Lys
 85 90 95
 Arg Tyr Ile Leu Gln Pro Ser Gly Leu Lys Val Gly Asp Ser Val Ile
 100 105 110
 Ala Ala Glu Gly Gly Leu Asp Ile Lys Val Gly Phe Ala Met Lys Leu
 115 120 125
 Lys Asn Ile Pro Ile Gly Thr Val Val His Asn Ile Glu Met His Pro
 130 135 140
 Gly Ala Gly Gly Gln Leu Ala Arg Ser Ala Gly Met Ser Ala Gln Ile
 145 150 155 160
 Met Gly Arg Glu Asn Lys Tyr Thr Ile Ile Arg Met Pro Ser Ser Glu
 165 170 175
 Met Arg Tyr Ile Leu Ser Glu Cys Met Ala Ser Val Gly Val Val Gly
 180 185 190
 Asn Glu Asp Phe Ile Asn Val Ser Ile Gly Lys Ala Gly Arg Asn Arg
 195 200 205
 His Arg Gly Ile Arg Pro Gln Thr Arg Gly Ser Ala Met Asn Pro Val
 210 215 220
 Asp His Pro His Gly Gly Glu
 225 230

<210> 131

<211> 528

<212> DNA

<213> Helicobacter pylori

<220>

<221> CDS

<222> (1)..(528)

<400> 131

tac gat tgg atc aag gaa ttt gtg cgc gat caa gga gag ttt atc gcc 48

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Tyr Asp Trp Ile Lys Glu Phe Val Arg Asp Gln Gly Glu Phe Ile Ala
 1          5          10          15
caa caa agc ggg tgg ctg gaa tta gag cga tca agc tat gcc aaa ctc 96
Gln Gln Ser Gly Trp Leu Glu Leu Glu Arg Ser Ser Tyr Ala Lys Leu
          20          25          30
atc gcg caa acc atc tcg cat gtg ctt aat ggc gga tcg ctg ttg gtg 144
Ile Ala Gln Thr Ile Ser His Val Leu Asn Gly Gly Ser Leu Leu Val
          35          40          45
agc gcg gat tct tct agg cac tgg ttt tta aac tac att ctt tct aac 192
Ser Ala Asp Ser Ser Arg His Trp Phe Leu Asn Tyr Ile Leu Ser Asn
          50          55          60
cta aac ccc aaa gat tta aaa gag cgc ccc tta ttg tcc gtc att gat 240
Leu Asn Pro Lys Asp Leu Lys Glu Arg Pro Leu Leu Ser Val Ile Asp
          65          70          75          80
ttt aac gct tct tct ttc tac ccc aaa aac gat gcg aat ctc tct cta 288
Phe Asn Ala Ser Ser Phe Tyr Pro Lys Asn Asp Ala Asn Leu Ser Leu
          85          90          95
gcc acc ata gag atg act tat caa aac ccc atg ttt tgg cat gtt ggg 336
Ala Thr Ile Glu Met Thr Tyr Gln Asn Pro Met Phe Trp His Val Gly
          100          105          110
aaa att gaa aat gaa ggc tta aaa acg ata cta ttg agt aaa atc cct 384
Lys Ile Glu Asn Glu Gly Leu Lys Thr Ile Leu Leu Ser Lys Ile Pro
          115          120          125
agt ttt tta tgg ctt ttt gaa gag ctt aaa gaa gat tgc ttg ctt tta 432
Ser Phe Leu Trp Leu Phe Glu Glu Leu Lys Glu Asp Cys Leu Leu Leu
          130          135          140
aaa gag cat gac agc ttg ctg gat tat aaa tta ttg cag ctc ttc aaa 480
Lys Glu His Asp Ser Leu Leu Asp Tyr Lys Leu Leu Gln Leu Phe Lys
          145          150          155          160
ctc ttt gaa aac gcg ctt ttt agc gtg cta tac aat aag gtt act ctg 528
Leu Phe Glu Asn Ala Leu Phe Ser Val Leu Tyr Asn Lys Val Thr Leu
          165          170          175

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<210> 132

<211> 176

<212> PRT

<213> *Helicobacter pylori*

<400> 132

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Tyr Asp Trp Ile Lys Glu Phe Val Arg Asp Gln Gly Glu Phe Ile Ala
 1          5          10          15
Gln Gln Ser Gly Trp Leu Glu Leu Glu Arg Ser Ser Tyr Ala Lys Leu
          20          25          30
Ile Ala Gln Thr Ile Ser His Val Leu Asn Gly Gly Ser Leu Leu Val
          35          40          45
Ser Ala Asp Ser Ser Arg His Trp Phe Leu Asn Tyr Ile Leu Ser Asn
          50          55          60
Leu Asn Pro Lys Asp Leu Lys Glu Arg Pro Leu Leu Ser Val Ile Asp
          65          70          75          80
Phe Asn Ala Ser Ser Phe Tyr Pro Lys Asn Asp Ala Asn Leu Ser Leu
          85          90          95
Ala Thr Ile Glu Met Thr Tyr Gln Asn Pro Met Phe Trp His Val Gly
          100          105          110
Lys Ile Glu Asn Glu Gly Leu Lys Thr Ile Leu Leu Ser Lys Ile Pro
          115          120          125
Ser Phe Leu Trp Leu Phe Glu Glu Leu Lys Glu Asp Cys Leu Leu Leu
          130          135          140
Lys Glu His Asp Ser Leu Leu Asp Tyr Lys Leu Leu Gln Leu Phe Lys
          145          150          155          160
Leu Phe Glu Asn Ala Leu Phe Ser Val Leu Tyr Asn Lys Val Thr Leu
          165          170          175

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<210> 133

<211> 263

<212> DNA

<213> Helicobacter pylori

<220>

<221> CDS

<222> (1)..(261)

<400> 133

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ttg gcg cta gtc aaa caa aat cct aaa gtt agt ctc ata gag tat gaa 48
Leu Ala Leu Val Lys Gln Asn Pro Lys Val Ser Leu Ile Glu Tyr Glu
1 5 10 15
aat tac ttt agc caa ctc aaa tac aac cct aac gca agc aag agc gat 96
Asn Tyr Phe Ser Gln Leu Lys Tyr Asn Pro Asn Ala Ser Lys Ser Asp
20 25 30
att gcc ttt ttt tat gcc ccc aac caa gtc tta tgc acc acg att aca 144
Ile Ala Phe Phe Tyr Ala Pro Asn Gln Val Leu Cys Thr Thr Ile Thr
35 40 45
gct aaa tac gcc gcg ttg ctt aaa gaa att tta agc cag aat aaa gtc 192
Ala Lys Tyr Gly Ala Leu Leu Lys Glu Ile Leu Ser Gln Asn Lys Val
50 55 60
ggc atg cat tta gcc cac agc gtg gat gtg cgt att gaa gta gcg cct 240
Gly Met His Leu Ala His Ser Val Asp Val Arg Ile Glu Val Ala Pro
65 70 75 80
aaa atc caa att aac gcc caa tc 263
Lys Ile Gln Ile Asn Ala Gln
85

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<210> 134

<211> 87

<212> PRT

<213> Helicobacter pylori

<400> 134

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Leu Ala Leu Val Lys Gln Asn Pro Lys Val Ser Leu Ile Glu Tyr Glu
1 5 10 15
Asn Tyr Phe Ser Gln Leu Lys Tyr Asn Pro Asn Ala Ser Lys Ser Asp
20 25 30
Ile Ala Phe Phe Tyr Ala Pro Asn Gln Val Leu Cys Thr Thr Ile Thr
35 40 45
Ala Lys Tyr Gly Ala Leu Leu Lys Glu Ile Leu Ser Gln Asn Lys Val
50 55 60
Gly Met His Leu Ala His Ser Val Asp Val Arg Ile Glu Val Ala Pro
65 70 75 80
Lys Ile Gln Ile Asn Ala Gln
85

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<210> 135

<211> 447

<212> DNA

<213> Helicobacter pylori

<220>

<221> CDS

<222> (1)..(447)

<400> 135

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agc tat gcc aaa ctc atc gcg caa acc atc tcg cat gtg ctt aat ggc 48
Ser Tyr Ala Lys Leu Ile Ala Gln Thr Ile Ser His Val Leu Asn Gly
1 5 10 15
gga tcg ctg ttg gtg agc gcg gat tct tct agg cac tgg ttt tta aac 96
Gly Ser Leu Leu Val Ser Ala Asp Ser Ser Arg His Trp Phe Leu Asn
20 25 30
tac att ctt tct aac cta aac ccc aaa gat tta aaa gag cgc ccc tta 144
Tyr Ile Leu Ser Asn Leu Asn Pro Lys Asp Leu Lys Glu Arg Pro Leu
35 40 45
ttg tcc gtc att gat ttt aac gct tct tct ttc tac ccc aaa aac gat 192
Leu Ser Val Ile Asp Phe Asn Ala Ser Ser Phe Tyr Pro Lys Asn Asp
50 55 60

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gcg aat ctc tct cta gcc acc ata gag atg act tat caa aac ccc atg 240
 Ala Asn Leu Ser Leu Ala Thr Ile Glu Met Thr Tyr Gln Asn Pro Met
 65 70 75 80
 ttt tgg cat gtt ggg aaa att gaa aat gaa ggc tta aaa acg ata cta 288
 Phe Trp His Val Gly Lys Ile Glu Asn Glu Gly Leu Lys Thr Ile Leu
 85 90 95
 ttg agt aaa atc cct agt ttt tta tgg ctt ttt gaa gag ctt aaa gaa 336
 Leu Ser Lys Ile Pro Ser Phe Leu Trp Leu Phe Glu Glu Leu Lys Glu
 100 105 110
 gat tgc ttg ctt tta aaa gag cat gac agc ttg ctg gat tat aaa tta 384
 Asp Cys Leu Leu Leu Lys Glu His Asp Ser Leu Leu Asp Tyr Lys Leu
 115 120 125
 ttg cag ctc ttc aaa ctc ttt gaa aac gcg ctt ttt agc gtg cta tac 432
 Leu Gln Leu Phe Lys Leu Phe Glu Asn Ala Leu Phe Ser Val Leu Tyr
 130 135 140
 aat aag gtt act ctg 447
 Asn Lys Val Thr Leu
 145
 <210> 136
 <211> 149
 <212> PRT
 <213> Helicobacter pylori
 <400> 136
 Ser Tyr Ala Lys Leu Ile Ala Gln Thr Ile Ser His Val Leu Asn Gly
 1 5 10 15
 Gly Ser Leu Leu Val Ser Ala Asp Ser Ser Arg His Trp Phe Leu Asn
 20 25 30
 Tyr Ile Leu Ser Asn Leu Asn Pro Lys Asp Leu Lys Glu Arg Pro Leu
 35 40 45
 Leu Ser Val Ile Asp Phe Asn Ala Ser Ser Phe Tyr Pro Lys Asn Asp
 50 55 60
 Ala Asn Leu Ser Leu Ala Thr Ile Glu Met Thr Tyr Gln Asn Pro Met
 65 70 75 80
 Phe Trp His Val Gly Lys Ile Glu Asn Glu Gly Leu Lys Thr Ile Leu
 85 90 95
 Leu Ser Lys Ile Pro Ser Phe Leu Trp Leu Phe Glu Glu Leu Lys Glu
 100 105 110
 Asp Cys Leu Leu Leu Lys Glu His Asp Ser Leu Leu Asp Tyr Lys Leu
 115 120 125
 Leu Gln Leu Phe Lys Leu Phe Glu Asn Ala Leu Phe Ser Val Leu Tyr
 130 135 140
 Asn Lys Val Thr Leu
 145
 <210> 137
 <211> 795
 <212> DNA
 <213> Helicobacter pylori
 <220>
 <221> CDS
 <222> (1)..(795)
 <400> 137
 gga ctt gga gga ggg act ggg act gga gcc acc cct act atc gtt aaa 48
 Gly Leu Gly Gly Gly Thr Gly Thr Gly Ala Thr Pro Thr Ile Val Lys
 1 5 10 15
 atc gca aaa gaa gtg gga gcg ctc acg att gct atc gtt acc aag cct 96
 Ile Ala Lys Glu Val Gly Ala Leu Thr Ile Ala Ile Val Thr Lys Pro
 20 25 30
 ttc aaa tac gaa ggg aat caa aaa aga aag agg gct gaa gag gga ttg 144
 Phe Lys Tyr Glu Gly Asn Gln Lys Arg Lys Arg Ala Glu Glu Gly Leu
 35 40 45
 aaa gaa ttg gag cag tct agc gat tct att ttg gtt atc cct aat gac 192

Lys Glu Leu Glu Gln Ser Ser Asp Ser Ile Leu Val Ile Pro Asn Asp
 50 55 60
 aaa atc ctt ctc acc atg aaa aaa aac gct agc acc acg gag tgt tat 240
 Lys Ile Leu Leu Thr Met Lys Lys Asn Ala Ser Thr Thr Glu Cys Tyr
 65 70 75 80
 agg gaa gtt gat gat gtc ttg gtt agg gct gtg agt ggc att tct act 288
 Arg Glu Val Asp Asp Val Leu Val Arg Ala Val Ser Gly Ile Ser Thr
 85 90 95
 atc atc act aaa ccc ggt aat atc aat gtt gat ttt gcc gat tta aag 336
 Ile Ile Thr Lys Pro Gly Asn Ile Asn Val Asp Phe Ala Asp Leu Lys
 100 105 110
 agc gct ctt ggt ttt aaa ggc ttt gcg tta atg ggt att ggt gaa gcc 384
 Ser Ala Leu Gly Phe Lys Gly Phe Ala Leu Met Gly Ile Gly Glu Ala
 115 120 125
 act ggc gaa gaa tcc gct aaa tta gcg gtg caa aat gcg atc caa tcg 432
 Thr Gly Glu Glu Ser Ala Lys Leu Ala Val Gln Asn Ala Ile Gln Ser
 130 135 140
 cct ctt ctt gat gac gct tct att gaa ggg gct aag agc att att gtc 480
 Pro Leu Leu Asp Asp Ala Ser Ile Glu Gly Ala Lys Ser Ile Ile Val
 145 150 155 160
 ttt ttt gag cac cac cct gat tat cct atg atg gct tat tct caa gcg 528
 Phe Phe Glu His His Pro Asp Tyr Pro Met Met Ala Tyr Ser Gln Ala
 165 170 175
 tgc gat ttt att caa gat caa gcc cat caa gat gtt gac gtt aag ttt 576
 Cys Asp Phe Ile Gln Asp Gln Ala His Gln Asp Val Asp Val Lys Phe
 180 185 190
 ggc caa cac acg agc gat aat atc cct att gat cat gtg cgc gtt act 624
 Gly Gln His Thr Ser Asp Asn Ile Pro Ile Asp His Val Arg Val Thr
 195 200 205
 atc att gca acc ggt gct gaa aga aac agc ggt gga gcg agt ttg gaa 672
 Ile Ile Ala Thr Gly Ala Glu Arg Asn Ser Gly Gly Ala Ser Leu Glu
 210 215 220
 tct atc gct acg ccc tct cag cct gtg gtg aaa caa acg aga aaa gtg 720
 Ser Ile Ala Thr Pro Ser Gln Pro Val Val Lys Gln Thr Arg Lys Val
 225 230 235 240
 ggt aat ggc gag tat tta aag atc cct act gaa gaa gag cta tcc ata 768
 Gly Asn Gly Glu Tyr Leu Lys Ile Pro Thr Glu Glu Glu Leu Ser Ile
 245 250 255
 ccc aca acc atg aga atc cag caa gac 795
 Pro Thr Thr Met Arg Ile Gln Gln Asp
 260 265

<210> 138

<211> 265

<212> PRT

<213> *Helicobacter pylori*

<400> 138

Gly Leu Gly Gly Gly Thr Gly Thr Gly Ala Thr Pro Thr Ile Val Lys
 1 5 10 15
 Ile Ala Lys Glu Val Gly Ala Leu Thr Ile Ala Ile Val Thr Lys Pro
 20 25 30
 Phe Lys Tyr Glu Gly Asn Gln Lys Arg Lys Arg Ala Glu Glu Gly Leu
 35 40 45
 Lys Glu Leu Glu Gln Ser Ser Asp Ser Ile Leu Val Ile Pro Asn Asp
 50 55 60
 Lys Ile Leu Leu Thr Met Lys Lys Asn Ala Ser Thr Thr Glu Cys Tyr
 65 70 75 80
 Arg Glu Val Asp Asp Val Leu Val Arg Ala Val Ser Gly Ile Ser Thr
 85 90 95
 Ile Ile Thr Lys Pro Gly Asn Ile Asn Val Asp Phe Ala Asp Leu Lys
 100 105 110
 Ser Ala Leu Gly Phe Lys Gly Phe Ala Leu Met Gly Ile Gly Glu Ala

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      115      120      125
Thr Gly Glu Glu Ser Ala Lys Leu Ala Val Gln Asn Ala Ile Gln Ser
      130      135      140
Pro Leu Leu Asp Asp Ala Ser Ile Glu Gly Ala Lys Ser Ile Ile Val
145      150      155      160
Phe Phe Glu His His Pro Asp Tyr Pro Met Met Ala Tyr Ser Gln Ala
      165      170      175
Cys Asp Phe Ile Gln Asp Gln Ala His Gln Asp Val Asp Val Lys Phe
      180      185      190
Gly Gln His Thr Ser Asp Asn Ile Pro Ile Asp His Val Arg Val Thr
      195      200      205
Ile Ile Ala Thr Gly Ala Glu Arg Asn Ser Gly Gly Ala Ser Leu Glu
210      215      220
Ser Ile Ala Thr Pro Ser Gln Pro Val Val Lys Gln Thr Arg Lys Val
225      230      235      240
Gly Asn Gly Glu Tyr Leu Lys Ile Pro Thr Glu Glu Glu Leu Ser Ile
      245      250      255
Pro Thr Thr Met Arg Ile Gln Gln Asp
      260      265

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<210> 139

<211> 342

<212> DNA

<213> Helicobacter pylori

<220>

<221> CDS

<222> (1)..(342)

<400> 139

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gcg gtt tct caa ctc att caa gtg gga gcg tta gtc aag ttt ttg tta 48
Ala Val Ser Gln Leu Ile Gln Val Gly Ala Leu Val Lys Phe Leu Leu
1      5      10      15
gcg ttt caa aaa agc act caa gct aaa atc gtt caa gtg tgt ggt ttt 96
Ala Phe Gln Lys Ser Thr Gln Ala Lys Ile Val Gln Val Cys Gly Phe
      20      25      30
aac ccc cat gcg ggc gaa gag ggc tta ttt ggg gaa gaa gat gaa agg 144
Asn Pro His Ala Gly Glu Glu Gly Leu Phe Gly Glu Glu Asp Glu Arg
      35      40      45
att tta aaa gcc att caa aag agc aac caa acg cta ggc ttt gaa tgc 192
Ile Leu Lys Ala Ile Gln Lys Ser Asn Gln Thr Leu Gly Phe Glu Cys
      50      55      60
ttt ttg ggg cca ctg ccg gct gat agt gct ttt gcc ccc aat aaa cga 240
Phe Leu Gly Pro Leu Pro Ala Asp Ser Ala Phe Ala Pro Asn Lys Arg
      65      70      75      80
aaa ata acc cct ttt tat gtg agc atg agc cat gat gtg ggg cta gcc 288
Lys Ile Thr Pro Phe Tyr Val Ser Met Ser His Asp Val Gly Leu Ala
      85      90      95
cct tta aaa gcg ctc tat ttt gat gaa agc att aat gtg agt ttg aac 336
Pro Leu Lys Ala Leu Tyr Phe Asp Glu Ser Ile Asn Val Ser Leu Asn
      100      105      110
gcc ccc
Ala Pro

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<210> 140

<211> 114

<212> PRT

<213> Helicobacter pylori

<400> 140

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Ala Val Ser Gln Leu Ile Gln Val Gly Ala Leu Val Lys Phe Leu Leu
1      5      10      15
Ala Phe Gln Lys Ser Thr Gln Ala Lys Ile Val Gln Val Cys Gly Phe
      20      25      30
Asn Pro His Ala Gly Glu Glu Gly Leu Phe Gly Glu Glu Asp Glu Arg
      35      40      45

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Ile Leu Lys Ala Ile Gln Lys Ser Asn Gln Thr Leu Gly Phe Glu Cys
 50 55 60
 Phe Leu Gly Pro Leu Pro Ala Asp Ser Ala Phe Ala Pro Asn Lys Arg
 65 70 75 80
 Lys Ile Thr Pro Phe Tyr Val Ser Met Ser His Asp Val Gly Leu Ala
 85 90 95
 Pro Leu Lys Ala Leu Tyr Phe Asp Glu Ser Ile Asn Val Ser Leu Asn
 100 105 110

Ala Pro

<210> 141

<211> 869

<212> DNA

<213> Helicobacter pylori

<220>

<221> CDS

<222> (1)..(867)

<400> 141

ggc ggg att gcg tgc gcg aat ttg ttg cat aaa aat tca ggg atc acg 48
 Gly Gly Ile Ala Cys Ala Asn Leu Leu His Lys Asn Ser Gly Ile Thr
 1 5 10 15
 ata gat att gga ggg ggt agc acc gag tgc gcg ttg att gaa aaa ggc 96
 Ile Asp Ile Gly Gly Gly Ser Thr Glu Cys Ala Leu Ile Glu Lys Gly
 20 25 30
 aag att aag gac tta atc tgc ctt gat gtt ggg acg att cgc att aaa 144
 Lys Ile Lys Asp Leu Ile Ser Leu Asp Val Gly Thr Ile Arg Ile Lys
 35 40 45
 gaa atg ttt tta gac aaa gac tta gag gtc aaa ttg gct aaa gcc ttt 192
 Glu Met Phe Leu Asp Lys Asp Leu Glu Val Lys Leu Ala Lys Ala Phe
 50 55 60
 atc caa aaa gaa gtc tct aaa ctg ccc ttt aaa cac aaa aac gcc ttt 240
 Ile Gln Lys Glu Val Ser Lys Leu Pro Phe Lys His Lys Asn Ala Phe
 65 70 75 80
 ggg gtg ggg ggg acg atc aga gcg ttg agt aag gta ttg atg aaa cgc 288
 Gly Val Gly Gly Thr Ile Arg Ala Leu Ser Lys Val Leu Met Lys Arg
 85 90 95
 ttt tgt tac cct att gat tct ttg cat ggc tat gaa ata gat gca cat 336
 Phe Cys Tyr Pro Ile Asp Ser Leu His Gly Tyr Glu Ile Asp Ala His
 100 105 110
 aaa aat tta gcg ttc att gaa aaa atc gtc atg ctc aaa gaa gat caa 384
 Lys Asn Leu Ala Phe Ile Glu Lys Ile Val Met Leu Lys Glu Asp Gln
 115 120 125
 tta cgg ctt tta ggg gtg aat gaa gag cgt ttg gat agc atc agg agc 432
 Leu Arg Leu Leu Gly Val Asn Glu Glu Arg Leu Asp Ser Ile Arg Ser
 130 135 140
 ggg gcg ttg att tta tca gtc gtt ttg gag cat tta aaa act tct tta 480
 Gly Ala Leu Ile Leu Ser Val Val Leu Glu His Leu Lys Thr Ser Leu
 145 150 155 160
 atg atc act agt ggg gtg ggg gtg aga gaa ggc gtg ttt ttg agc gat 528
 Met Ile Thr Ser Gly Val Gly Val Arg Glu Gly Val Phe Leu Ser Asp
 165 170 175
 tta ttg cgc cat cat tac cat aaa ttc ccc ccc aat atc aac ccc tct 576
 Leu Leu Arg His His Tyr His Lys Phe Pro Pro Asn Ile Asn Pro Ser
 180 185 190
 ctc atc tct tta aaa gat cgc ttt ttg ccc cat gaa aag cac agc caa 624
 Leu Ile Ser Leu Lys Asp Arg Phe Leu Pro His Glu Lys His Ser Gln
 195 200 205
 aag gtc aaa aaa gaa tgc gtg aaa ttg ttt gaa gcc tta tgc cct ttg 672
 Lys Val Lys Lys Glu Cys Val Lys Leu Phe Glu Ala Leu Ser Pro Leu
 210 215 220
 cat aaa ata gat gaa aaa tac ctt ttc cat tta aag att gcg ggg gaa 720
 His Lys Ile Asp Glu Lys Tyr Leu Phe His Leu Lys Ile Ala Gly Glu

225	tta	gcg	agc	atg	ggt	aag	att	tta	agc	gtc	tat	tta	gcc	cac	aag	cac	240	
Leu	Ala	Ser	Met	Gly	Lys	Ile	Leu	Ser	Val	Tyr	Leu	Ala	His	Lys	His		768	
				245					250					255				
agc	gcg	tat	ttt	att	tta	aac	gct	ttg	agt	tat	ggc	ttt	agc	cac	cag		816	
Ser	Ala	Tyr	Phe	Ile	Leu	Asn	Ala	Leu	Ser	Tyr	Gly	Phe	Ser	His	Gln			
			260					265					270					
gat	aga	gcg	atc	att	tgc	tta	tta	gcc	caa	ttc	agc	cat	aaa	aaa	atc		864	
Asp	Arg	Ala	Ile	Ile	Cys	Leu	Leu	Ala	Gln	Phe	Ser	His	Lys	Lys	Ile			
			275				280					285						
cct	aa																869	
Pro																		
<210>	142																	
<211>	289																	
<212>	PRT																	
<213>	Helicobacter pylori																	
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Gly	Gly	Ile	Ala	Cys	Ala	Asn	Leu	Leu	His	Lys	Asn	Ser	Gly	Ile	Thr			
1				5					10					15				
Ile	Asp	Ile	Gly	Gly	Ser	Thr	Glu	Cys	Ala	Leu	Ile	Glu	Lys	Gly				
			20				25					30						
Lys	Ile	Lys	Asp	Leu	Ile	Ser	Leu	Asp	Val	Gly	Thr	Ile	Arg	Ile	Lys			
		35					40					45						
Glu	Met	Phe	Leu	Asp	Lys	Asp	Leu	Glu	Val	Lys	Leu	Ala	Lys	Ala	Phe			
	50					55					60							
Ile	Gln	Lys	Glu	Val	Ser	Lys	Leu	Pro	Phe	Lys	His	Lys	Asn	Ala	Phe			
	65				70				75						80			
Gly	Val	Gly	Gly	Thr	Ile	Arg	Ala	Leu	Ser	Lys	Val	Leu	Met	Lys	Arg			
				85					90					95				
Phe	Cys	Tyr	Pro	Ile	Asp	Ser	Leu	His	Gly	Tyr	Glu	Ile	Asp	Ala	His			
			100					105					110					
Lys	Asn	Leu	Ala	Phe	Ile	Glu	Lys	Ile	Val	Met	Leu	Lys	Glu	Asp	Gln			
	115						120					125						
Leu	Arg	Leu	Leu	Gly	Val	Asn	Glu	Glu	Arg	Leu	Asp	Ser	Ile	Arg	Ser			
	130					135					140							
Gly	Ala	Leu	Ile	Leu	Ser	Val	Val	Leu	Glu	His	Leu	Lys	Thr	Ser	Leu			
	145				150					155					160			
Met	Ile	Thr	Ser	Gly	Val	Gly	Val	Arg	Glu	Gly	Val	Phe	Leu	Ser	Asp			
				165					170						175			
Leu	Leu	Arg	His	His	Tyr	His	Lys	Phe	Pro	Pro	Asn	Ile	Asn	Pro	Ser			
			180					185					190					
Leu	Ile	Ser	Leu	Lys	Asp	Arg												

<400> 143

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Ser Leu Ile Ala Asn Ala Leu Leu Gln Ser Ser Phe Leu Leu Tyr Ala
1 5 10 15
ttc atg cca aag agc gct gtg aaa tta gcg aat gct ttc aac aca gaa 96
Phe Met Pro Lys Ser Ala Val Lys Leu Ala Asn Ala Phe Asn Thr Glu
20 25 30
atc acg ccc gat aat tac gaa cgc ttt ttt aaa gct aaa aaa tta caa 144
Ile Thr Pro Asp Asn Tyr Glu Arg Phe Phe Lys Ala Lys Lys Leu Gln
35 40 45
gat atg att tta caa gac acc gag cct tta ttt tcc aaa atg gag aaa 192
Asp Met Ile Leu Gln Asp Thr Glu Pro Leu Phe Ser Lys Met Glu Lys
50 55 60
att gaa aag acg gaa aaa gcg gga gaa gcc tca cca gaa aaa aac gaa 240
Ile Glu Lys Thr Glu Lys Ala Gly Glu Ala Ser Pro Glu Lys Asn Glu
65 70 75 80
aaa gaa aaa aag gac gca aaa gaa aaa gcc cca cta aaa caa gaa aac 288
Lys Glu Lys Lys Asp Ala Lys Glu Lys Ala Pro Leu Lys Gln Glu Asn
85 90 95
tat atc ggc att gag gat ttc aaa aaa gta gag atc aaa gtg ggg ctt 336
Tyr Ile Gly Ile Glu Asp Phe Lys Lys Val Glu Ile Lys Val Gly Leu
100 105 110
atc aaa gaa gct caa agg att gaa aaa tcc aat aaa tta ctg cgc tta 384
Ile Lys Glu Ala Gln Arg Ile Glu Lys Ser Asn Lys Leu Leu Arg Leu
115 120 125
aaa gtg gat tta ggc gaa ggc cgt ttg agg cag att att tca ggg atc 432
Lys Val Asp Leu Gly Glu Gly Arg Leu Arg Gln Ile Ile Ser Gly Ile
130 135 140
gct ttg gat tat gag cct gaa agc ttg gtg ggt caa atg gtg tgc gtg 480
Ala Leu Asp Tyr Glu Pro Glu Ser Leu Val Gly Gln Met Val Cys Val
145 150 155 160
gtg gct aat tta aaa ccc gca aag ctt atg ggc gaa atg agt gag ggc 528
Val Ala Asn Leu Lys Pro Ala Lys Leu Met Gly Glu Met Ser Glu Gly
165 170 175
atg att tta gcg gtg cga gat agc gac aat cta gcc tta att agc ccc 576
Met Ile Leu Ala Val Arg Asp Ser Asp Asn Leu Ala Leu Ile Ser Pro
180 185 190
act aga gaa aaa att gca gga agt ttg atc agc 609
Thr Arg Glu Lys Ile Ala Gly Ser Leu Ile Ser
195 200

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<210> 144

<211> 203

<212> PRT

<213> *Helicobacter pylori*

<400> 144

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Ser Leu Ile Ala Asn Ala Leu Leu Gln Ser Ser Phe Leu Leu Tyr Ala
1 5 10 15
Phe Met Pro Lys Ser Ala Val Lys Leu Ala Asn Ala Phe Asn Thr Glu
20 25 30
Ile Thr Pro Asp Asn Tyr Glu Arg Phe Phe Lys Ala Lys Lys Leu Gln
35 40 45
Asp Met Ile Leu Gln Asp Thr Glu Pro Leu Phe Ser Lys Met Glu Lys
50 55 60
Ile Glu Lys Thr Glu Lys Ala Gly Glu Ala Ser Pro Glu Lys Asn Glu
65 70 75 80
Lys Glu Lys Lys Asp Ala Lys Glu Lys Ala Pro Leu Lys Gln Glu Asn
85 90 95
Tyr Ile Gly Ile Glu Asp Phe Lys Lys Val Glu Ile Lys Val Gly Leu
100 105 110
Ile Lys Glu Ala Gln Arg Ile Glu Lys Ser Asn Lys Leu Leu Arg Leu
115 120 125

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Lys Val Asp Leu Gly Glu Gly Arg Leu Arg Gln Ile Ile Ser Gly Ile
 130 135 140
 Ala Leu Asp Tyr Glu Pro Glu Ser Leu Val Gly Gln Met Val Cys Val
 145 150 155 160
 Val Ala Asn Leu Lys Pro Ala Lys Leu Met Gly Glu Met Ser Glu Gly
 165 170 175
 Met Ile Leu Ala Val Arg Asp Ser Asp Asn Leu Ala Leu Ile Ser Pro
 180 185 190
 Thr Arg Glu Lys Ile Ala Gly Ser Leu Ile Ser
 195 200

<210> 145

<211> 1458

<212> DNA

<213> Helicobacter pylori

<220>

<221> CDS

<222> (1)..(1458)

<400> 145

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Phe Glu Asn Ala Lys Ala Glu Cys Ser Leu Val Phe Ile Ile Asn Lys	
1 5 10 15	
gat ttt agc cac gct tgg gtc aaa aat aaa gag ttg cta gaa acc ttt	96
Asp Phe Ser His Ala Trp Val Lys Asn Lys Glu Leu Leu Glu Thr Phe	
20 25 30	
aaa tac gaa ggc gaa ggc gta ttt tta gac caa gaa aat aaa atc ctg	144
Lys Tyr Glu Gly Glu Gly Val Phe Leu Asp Gln Glu Asn Lys Ile Leu	
35 40 45	
tat gcg ggc gtt aaa gaa gat gat gtg cat tta ttg aga gag agc gcg	192
Tyr Ala Gly Val Lys Glu Asp Asp Val His Leu Leu Arg Glu Ser Ala	
50 55 60	
tgt tta gcc gtt cgc acc ctt aaa aaa ctc gct ttt aaa agc gtt aaa	240
Cys Leu Ala Val Arg Thr Leu Lys Lys Leu Ala Phe Lys Ser Val Lys	
65 70 75 80	
gtg ggc gtt tat act tgt ggt gca cat tct aaa gat aac gcg ctt tta	288
Val Gly Val Tyr Thr Cys Gly Ala His Ser Lys Asp Asn Ala Leu Leu	
85 90 95	
gaa aac ttg aaa gcg ctg ttt ttg ggc ttg aaa tta ggt ttg tat gaa	336
Glu Asn Leu Lys Ala Leu Phe Leu Gly Leu Lys Leu Gly Leu Tyr Glu	
100 105 110	
tac gac act ttt aaa tcc aac aaa aaa gaa agc gtt tta aaa gaa gcc	384
Tyr Asp Thr Phe Lys Ser Asn Lys Lys Glu Ser Val Leu Lys Glu Ala	
115 120 125	
att gtc gct tta gaa ttg cac aaa cct tgc gaa aaa act tgc gca aat	432
Ile Val Ala Leu Glu Leu His Lys Pro Cys Glu Lys Thr Cys Ala Asn	
130 135 140	
tct tta gaa aag agt gct aaa gaa gcg tta aaa tac gct gaa atc atg	480
Ser Leu Glu Lys Ser Ala Lys Glu Ala Leu Lys Tyr Ala Glu Ile Met	
145 150 155 160	
aca gaa agc ttg aat atc gtt aaa gat cta gtc aat acc ccc cct atg	528
Thr Glu Ser Leu Asn Ile Val Lys Asp Leu Val Asn Thr Pro Pro Met	
165 170 175	
att ggc act ccg gtt tat atg gct gaa gtg gcg caa aaa gtg gct aaa	576
Ile Gly Thr Pro Val Tyr Met Ala Glu Val Ala Gln Lys Val Ala Lys	
180 185 190	
gaa aac cat tta gaa atc cat gtt cat gat gaa aaa ttt tta gaa gaa	624
Glu Asn His Leu Glu Ile His Val His Asp Glu Lys Phe Leu Glu Glu	
195 200 205	
aag aaa atg aac gcc ttt tta gcg gtc aat aaa gcc tct ctt agc gtc	672
Lys Lys Met Asn Ala Phe Leu Ala Val Asn Lys Ala Ser Leu Ser Val	
210 215 220	
aat cct cct cgc ttg atc cat tta gtc tat aag cct aaa aaa gcg aag	720

Asn Pro Pro Arg Leu Ile His Leu Val Tyr Lys Pro Lys Lys Ala Lys
 225 230 235 240
 aaa aaa atc gct tta gtg ggt aag ggc ttg act tat gat tgt ggg ggt 768
 Lys Lys Ile Ala Leu Val Gly Lys Gly Leu Thr Tyr Asp Cys Gly Gly
 245 250 255
 ttg agc ttg aaa ccg gcc gat tac atg gtt act atg aaa gcg gat aaa 816
 Leu Ser Leu Lys Pro Ala Asp Tyr Met Val Thr Met Lys Ala Asp Lys
 260 265 270
 ggc ggt ggc tct gcg gtg att ggg ctt tta aac gca tta gcc aaa cta 864
 Gly Gly Gly Ser Ala Val Ile Gly Leu Leu Asn Ala Leu Ala Lys Leu
 275 280 285
 ggc gtg gag gct gaa gtg cat ggc att att ggg gct aca gaa aac atg 912
 Gly Val Glu Ala Glu Val His Gly Ile Ile Gly Ala Thr Glu Asn Met
 290 295 300
 ata ggc cca gcc gct tat aaa cca gat gat att ttg atc tcc aaa gaa 960
 Ile Gly Pro Ala Ala Tyr Lys Pro Asp Asp Ile Leu Ile Ser Lys Glu
 305 310 315 320
 ggc aag agc ata gag gtc cgt aat acc gac gct gag ggg cgt ttg gtt 1008
 Gly Lys Ser Ile Glu Val Arg Asn Thr Asp Ala Glu Gly Arg Leu Val
 325 330 335
 tta gcg gat tgt ttg agc tac gct caa gat tta aac cct gat gtg atc 1056
 Leu Ala Asp Cys Leu Ser Tyr Ala Gln Asp Leu Asn Pro Asp Val Ile
 340 345 350
 gtg gat ttt gcg acc ctt act ggg gca tgc gtt gta ggc tta ggc gaa 1104
 Val Asp Phe Ala Thr Leu Thr Gly Ala Cys Val Val Gly Leu Gly Glu
 355 360 365
 ttc act tca gcg atc atg ggg cat aat gaa gag tta aaa aac ctc ttt 1152
 Phe Thr Ser Ala Ile Met Gly His Asn Glu Glu Leu Lys Asn Leu Phe
 370 375 380
 gaa act tca ggg tta gaa tcc ggc gaa tta tta gcc aaa ctc ccc ttt 1200
 Glu Thr Ser Gly Leu Glu Ser Gly Glu Leu Leu Ala Lys Leu Pro Phe
 385 390 395 400
 aac cgc cat tta aag aaa ttg att gaa tct aaa atc gct gat gtg tgc 1248
 Asn Arg His Leu Lys Lys Leu Ile Glu Ser Lys Ile Ala Asp Val Cys
 405 410 415
 aat att tct tct tca cgc tat ggc ggt gcg atc aca gcg ggc ttg ttt 1296
 Asn Ile Ser Ser Ser Arg Tyr Gly Gly Ala Ile Thr Ala Gly Leu Phe
 420 425 430
 tta aat gaa ttt att aga gat gag ttt aag gat aag tgg cta cac att 1344
 Leu Asn Glu Phe Ile Arg Asp Glu Phe Lys Asp Lys Trp Leu His Ile
 435 440 445
 gac att gca ggc cct gct tat gtg gaa aaa gaa tgg gat gtg aat agc 1392
 Asp Ile Ala Gly Pro Ala Tyr Val Glu Lys Glu Trp Asp Val Asn Ser
 450 455 460
 ttt gga gcg agt ggg gct ggc gtg aga gct tgc aca gct ttt gtg gaa 1440
 Phe Gly Ala Ser Gly Ala Gly Val Arg Ala Cys Thr Ala Phe Val Glu
 465 470 475 480
 gag ctt ttg aaa aag gct
 Glu Leu Leu Lys Lys Ala
 485

<210> 146

<211> 486

<212> PRT

<213> Helicobacter pylori

<400> 146

Phe Glu Asn Ala Lys Ala Glu Cys Ser Leu Val Phe Ile Ile Asn Lys
 1 5 10 15
 Asp Phe Ser His Ala Trp Val Lys Asn Lys Glu Leu Leu Glu Thr Phe
 20 25 30
 Lys Tyr Glu Gly Glu Gly Val Phe Leu Asp Gln Glu Asn Lys Ile Leu
 35 40 45

Tyr Ala Gly Val Lys Glu Asp Asp Val His Leu Leu Arg Glu Ser Ala
 50 55 60
 Cys Leu Ala Val Arg Thr Leu Lys Lys Leu Ala Phe Lys Ser Val Lys
 65 70 75 80
 Val Gly Val Tyr Thr Cys Gly Ala His Ser Lys Asp Asn Ala Leu Leu
 85 90 95
 Glu Asn Leu Lys Ala Leu Phe Leu Gly Leu Lys Leu Gly Leu Tyr Glu
 100 105 110
 Tyr Asp Thr Phe Lys Ser Asn Lys Lys Glu Ser Val Leu Lys Glu Ala
 115 120 125
 Ile Val Ala Leu Glu Leu His Lys Pro Cys Glu Lys Thr Cys Ala Asn
 130 135 140
 Ser Leu Glu Lys Ser Ala Lys Glu Ala Leu Lys Tyr Ala Glu Ile Met
 145 150 155 160
 Thr Glu Ser Leu Asn Ile Val Lys Asp Leu Val Asn Thr Pro Pro Met
 165 170 175
 Ile Gly Thr Pro Val Tyr Met Ala Glu Val Ala Gln Lys Val Ala Lys
 180 185 190
 Glu Asn His Leu Glu Ile His Val His Asp Glu Lys Phe Leu Glu Glu
 195 200 205
 Lys Lys Met Asn Ala Phe Leu Ala Val Asn Lys Ala Ser Leu Ser Val
 210 215 220
 Asn Pro Pro Arg Leu Ile His Leu Val Tyr Lys Pro Lys Lys Ala Lys
 225 230 235 240
 Lys Lys Ile Ala Leu Val Gly Lys Gly Leu Thr Tyr Asp Cys Gly Gly
 245 250 255
 Leu Ser Leu Lys Pro Ala Asp Tyr Met Val Thr Met Lys Ala Asp Lys
 260 265 270
 Gly Gly Gly Ser Ala Val Ile Gly Leu Leu Asn Ala Leu Ala Lys Leu
 275 280 285
 Gly Val Glu Ala Glu Val His Gly Ile Ile Gly Ala Thr Glu Asn Met
 290 295 300
 Ile Gly Pro Ala Ala Tyr Lys Pro Asp Asp Ile Leu Ile Ser Lys Glu
 305 310 315 320
 Gly Lys Ser Ile Glu Val Arg Asn Thr Asp Ala Glu Gly Arg Leu Val
 325 330 335
 Leu Ala Asp Cys Leu Ser Tyr Ala Gln Asp Leu Asn Pro Asp Val Ile
 340 345 350
 Val Asp Phe Ala Thr Leu Thr Gly Ala Cys Val Val Gly Leu Gly Glu
 355 360 365
 Phe Thr Ser Ala Ile Met Gly His Asn Glu Glu Leu Lys Asn Leu Phe
 370 375 380
 Glu Thr Ser Gly Leu Glu Ser Gly Glu Leu Leu Ala Lys Leu Pro Phe
 385 390 395 400
 Asn Arg His Leu Lys Lys Leu Ile Glu Ser Lys Ile Ala Asp Val Cys
 405 410 415
 Asn Ile Ser Ser Ser Arg Tyr Gly Gly Ala Ile Thr Ala Gly Leu Phe
 420 425 430
 Leu Asn Glu Phe Ile Arg Asp Glu Phe Lys Asp Lys Trp Leu His Ile
 435 440 445
 Asp Ile Ala Gly Pro Ala Tyr Val Glu Lys Glu Trp Asp Val Asn Ser
 450 455 460
 Phe Gly Ala Ser Gly Ala Gly Val Arg Ala Cys Thr Ala Phe Val Glu
 465 470 475 480
 Glu Leu Leu Lys Lys Ala
 485

<210> 147

<211> 960

<212> DNA

<213> Helicobacter pylori

<220>

<221> CDS

<222> (1)..(960)

<400> 147

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Asp Val Ile Lys Lys Val Thr Thr Pro Lys Gly Gly Ile Glu Ile Leu	
1 5 10 15	
agg act tta att gat ttt acg ccc aaa att gaa aac gcc ctg aat tta	96
Arg Thr Leu Ile Asp Phe Thr Pro Lys Ile Glu Asn Ala Leu Asn Leu	
20 25 30	
gcg gcc aaa agc cat aag ggg caa tac aga aaa agc ggc gag cct tat	144
Ala Ala Lys Ser His Lys Gly Gln Tyr Arg Lys Ser Gly Glu Pro Tyr	
35 40 45	
att gtc cat cct att tgc gtg gca agc ttg gta gcg ttt tgt ggg ggc	192
Ile Val His Pro Ile Cys Val Ala Ser Leu Val Ala Phe Cys Gly Gly	
50 55 60	
gat gag gcg atg gtg tgt gct gcg ctt ttg cat gat gtg gtg gaa gac	240
Asp Glu Ala Met Val Cys Ala Ala Leu Leu His Asp Val Val Glu Asp	
65 70 75 80	
acg cct tgt aag att gaa acg att gag caa gaa ttt ggg caa gat gtg	288
Thr Pro Cys Lys Ile Glu Thr Ile Glu Gln Glu Phe Gly Gln Asp Val	
85 90 95	
gct aat tta gtg gat gcg ctc act aaa atc act gaa atc agg aaa gaa	336
Ala Asn Leu Val Asp Ala Leu Thr Lys Ile Thr Glu Ile Arg Lys Glu	
100 105 110	
gaa tta ggc gtg agc tct caa gat ccc aga atg gtg gtt tca gcg ctc	384
Glu Leu Gly Val Ser Ser Gln Asp Pro Arg Met Val Val Ser Ala Leu	
115 120 125	
act ttc aga aag att tta att agc gcg ata caa gat cca aga gcc tta	432
Thr Phe Arg Lys Ile Leu Ile Ser Ala Ile Gln Asp Pro Arg Ala Leu	
130 135 140	
gtg gta aag att agc gac agg ttg cac aac atg ctc acc tta gac gcc	480
Val Val Lys Ile Ser Asp Arg Leu His Asn Met Leu Thr Leu Asp Ala	
145 150 155 160	
ttg cct cat gac aag caa gtg cgt att tct aaa gag act cta gcg gtg	528
Leu Pro His Asp Lys Gln Val Arg Ile Ser Lys Glu Thr Leu Ala Val	
165 170 175	
tat gcc cct ata gcg agc cga ttg ggc atg tct tca atc aaa aat gaa	576
Tyr Ala Pro Ile Ala Ser Arg Leu Gly Met Ser Ser Ile Lys Asn Glu	
180 185 190	
tta gaa gac aag agc ttt tat tat att tat cca gaa gag tat aaa aat	624
Leu Glu Asp Lys Ser Phe Tyr Tyr Ile Tyr Pro Glu Glu Tyr Lys Asn	
195 200 205	
atc aag gaa tat ttg cac aaa aac aag cag tct tta ctc tta aag ctc	672
Ile Lys Glu Tyr Leu His Lys Asn Lys Gln Ser Leu Leu Leu Lys Leu	
210 215 220	
aac gct ttt gcg agc aag tta gaa aaa aaa ctt ttt gat agt ggg ttt	720
Asn Ala Phe Ala Ser Lys Leu Glu Lys Lys Leu Phe Asp Ser Gly Phe	
225 230 235 240	
agc cat tcg gat ttt aaa ctc gtt aca agg gtg aaa cgc cct tat tct	768
Ser His Ser Asp Phe Lys Leu Val Thr Arg Val Lys Arg Pro Tyr Ser	
245 250 255	
atc tat ctt aag atg caa cga aag ggc gcg gtt aat att gat gaa att	816
Ile Tyr Leu Lys Met Gln Arg Lys Gly Ala Val Asn Ile Asp Glu Ile	
260 265 270	
ttg gac ttg tta gcc att agg att tta ttg aaa aac ccg att gat tgc	864
Leu Asp Leu Leu Ala Ile Arg Ile Leu Leu Lys Asn Pro Ile Asp Cys	
275 280 285	
tat aaa gtt tta ggg att atc cat ttg aat ttc aaa ccc att gtc tct	912
Tyr Lys Val Leu Gly Ile Ile His Leu Asn Phe Lys Pro Ile Val Ser	
290 295 300	
cgt ttt aaa gat tac atc gct ttg ccc aaa gaa aat ggc tat aag acg	960

Arg Phe Lys Asp Tyr Ile Ala Leu Pro Lys Glu Asn Gly Tyr Lys Thr
 305 310 315 320
 <210> 148
 <211> 320
 <212> PRT
 <213> *Helicobacter pylori*
 <400> 148
 Asp Val Ile Lys Lys Val Thr Thr Pro Lys Gly Gly Ile Glu Ile Leu
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 Arg Thr Leu Ile Asp Phe Thr Pro Lys Ile Glu Asn Ala Leu Asn Leu
 20 25 30
 Ala Ala Lys Ser His Lys Gly Gln Tyr Arg Lys Ser Gly Glu Pro Tyr
 35 40 45
 Ile Val His Pro Ile Cys Val Ala Ser Leu Val Ala Phe Cys Gly Gly
 50 55 60
 Asp Glu Ala Met Val Cys Ala Ala Leu Leu His Asp Val Val Glu Asp
 65 70 75 80
 Thr Pro Cys Lys Ile Glu Thr Ile Glu Gln Glu Phe Gly Gln Asp Val
 85 90 95
 Ala Asn Leu Val Asp Ala Leu Thr Lys Ile Thr Glu Ile Arg Lys Glu
 100 105 110
 Glu Leu Gly Val Ser Ser Gln Asp Pro Arg Met Val Val Ser Ala Leu
 115 120 125
 Thr Phe Arg Lys Ile Leu Ile Ser Ala Ile Gln Asp Pro Arg Ala Leu
 130 135 140
 Val Val Lys Ile Ser Asp Arg Leu His Asn Met Leu Thr Leu Asp Ala
 145 150 155 160
 Leu Pro His Asp Lys Gln Val Arg Ile Ser Lys Glu Thr Leu Ala Val
 165 170 175
 Tyr Ala Pro Ile Ala Ser Arg Leu Gly Met Ser Ser Ile Lys Asn Glu
 180 185 190
 Leu Glu Asp Lys Ser Phe Tyr Tyr Ile Tyr Pro Glu Glu Tyr Lys Asn
 195 200 205
 Ile Lys Glu Tyr Leu His Lys Asn Lys Gln Ser Leu Leu Lys Leu
 210 215 220
 Asn Ala Phe Ala Ser Lys Leu Glu Lys Lys Leu Phe Asp Ser Gly Phe
 225 230 235 240
 Ser His Ser Asp Phe Lys Leu Val Thr Arg Val Lys Arg Pro Tyr Ser
 245 250 255
 Ile Tyr Leu Lys Met Gln Arg Lys Gly Ala Val Asn Ile Asp Glu Ile
 260 265 270
 Leu Asp Leu Leu Ala Ile Arg Ile Leu Leu Lys Asn Pro Ile Asp Cys
 275 280 285
 Tyr Lys Val Leu Gly Ile Ile His Leu Asn Phe Lys Pro Ile Val Ser
 290 295 300
 Arg Phe Lys Asp Tyr Ile Ala Leu Pro Lys Glu Asn Gly Tyr Lys Thr
 305 310 315 320
 <210> 149
 <211> 324
 <212> DNA
 <213> *Helicobacter pylori*
 <220>
 <221> CDS
 <222> (1)..(324)
 <400> 149
 ttg cta gcg att gtg ttg agc att tct act ttt att gca caa ggt aag 48
 Leu Leu Ala Ile Val Leu Ser Ile Ser Thr Phe Ile Ala Gln Gly Lys
 1 5 10 15
 att aag gtc agt ctc cct aac gct aaa aat gcg gaa aaa tcc cag cca 96
 Ile Lys Val Ser Leu Pro Asn Ala Lys Asn Ala Glu Lys Ser Gln Pro
 20 25 30

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aac gat caa aaa gtg gtg gtc atc tct gta gat gag cat gac aat att 144
Asn Asp Gln Lys Val Val Val Ile Ser Val Asp Glu His Asp Asn Ile
      35              40              45
ttc gta gat gac aaa ccg atg aat tta gaa gct ttg agc gct gta gtc 192
Phe Val Asp Asp Lys Pro Met Asn Leu Glu Ala Leu Ser Ala Val Val
      50              55              60
aaa caa aca gac cct aaa acc ctt ata gac tta aaa agc gac aaa agc 240
Lys Gln Thr Asp Pro Lys Thr Leu Ile Asp Leu Lys Ser Asp Lys Ser
      65              70              75              80
tct cgt ttt gaa act ttt atc agc att atg gat att tta aaa gag cat 288
Ser Arg Phe Glu Thr Phe Ile Ser Ile Met Asp Ile Leu Lys Glu His
      85              90              95
aat cat gaa aat ttc tcc atc tcc acg caa gct cag 324
Asn His Glu Asn Phe Ser Ile Ser Thr Gln Ala Gln
      100              105

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<210> 150

<211> 108

<212> PRT

<213> Helicobacter pylori

<400> 150

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Leu Leu Ala Ile Val Leu Ser Ile Ser Thr Phe Ile Ala Gln Gly Lys
 1              5              10              15
Ile Lys Val Ser Leu Pro Asn Ala Lys Asn Ala Glu Lys Ser Gln Pro
      20              25              30
Asn Asp Gln Lys Val Val Val Ile Ser Val Asp Glu His Asp Asn Ile
      35              40              45
Phe Val Asp Asp Lys Pro Met Asn Leu Glu Ala Leu Ser Ala Val Val
      50              55              60
Lys Gln Thr Asp Pro Lys Thr Leu Ile Asp Leu Lys Ser Asp Lys Ser
      65              70              75              80
Ser Arg Phe Glu Thr Phe Ile Ser Ile Met Asp Ile Leu Lys Glu His
      85              90              95
Asn His Glu Asn Phe Ser Ile Ser Thr Gln Ala Gln
      100              105

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<210> 151

<211> 837

<212> DNA

<213> Helicobacter pylori

<220>

<221> CDS

<222> (1)..(837)

<400> 151

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gac agc aaa aaa gac gct tgc ggg ttc atc tat gag atc agc gag ttc 48
Asp Ser Lys Lys Asp Ala Cys Gly Phe Ile Tyr Glu Ile Ser Glu Phe
 1              5              10              15
atg aaa gcc tat acc gca ttg cta aaa aaa caa gac cga tac gtc tat 96
Met Lys Ala Tyr Thr Ala Leu Lys Lys Gln Asp Arg Tyr Val Tyr
      20              25              30
tta ttg agg tat ctc ccc tct agg tat tgg gcc agc att tta acg act 144
Leu Leu Arg Tyr Leu Pro Ser Arg Tyr Trp Ala Ser Ile Leu Thr Thr
      35              40              45
gcc ctt tat gtc aaa tac cct gat ttt gac gct ttg aaa aag ctt ttg 192
Ala Leu Tyr Val Lys Tyr Pro Asp Phe Asp Ala Leu Lys Lys Leu Leu
      50              55              60
gtg tct tat tat tac caa act tgg att gca gga ggc acg atc acg cgc 240
Val Ser Tyr Tyr Tyr Gln Thr Trp Ile Ala Gly Gly Thr Ile Thr Arg
      65              70              75              80
atc aag caa acc agt atc aac att atc aaa aac gtt aaa agc aat aag 288
Ile Lys Gln Thr Ser Ile Asn Ile Ile Lys Asn Val Lys Ser Asn Lys
      85              90              95
agc gtt gaa acc atc aaa gag ctt ata ttg aat agc atc gac tct tat 336

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Ser Val Glu Thr Ile Lys Glu Leu Ile Leu Asn Ser Ile Asp Ser Tyr
 100 105 110
 aac acc ttt gat caa tac ctc tat aac tta tgg gat agc tct tct gtt 384
 Asn Thr Phe Asp Gln Tyr Leu Tyr Asn Leu Trp Asp Ser Ser Ser Val
 115 120 125
 tat cat agc aaa tgg gtg cgt cct gtc tta gcc cta gct aat tat ttc 432
 Tyr His Ser Lys Trp Val Arg Pro Val Leu Ala Leu Ala Asn Tyr Phe
 130 135 140
 atg gca gat gaa gag aaa ccc cat ttt atc gct atg gat gcc gaa acc 480
 Met Ala Asp Glu Glu Lys Pro His Phe Ile Ala Met Asp Ala Glu Thr
 145 150 155 160
 caa gtg gag cat att ttg cca caa acg ccc aaa aga ggc agt caa tgg 528
 Gln Val Glu His Ile Leu Pro Gln Thr Pro Lys Arg Gly Ser Gln Trp
 165 170 175
 aac gcg gat ttt gac aaa gaa aaa aga gaa gaa tgg gta aat aat atc 576
 Asn Ala Asp Phe Asp Lys Glu Lys Arg Glu Glu Trp Val Asn Asn Ile
 180 185 190
 gcg aat tta acc ctt tta aag cgt aaa aag aac gcg cat gct tta aac 624
 Ala Asn Leu Thr Leu Leu Lys Arg Lys Lys Asn Ala His Ala Leu Asn
 195 200 205
 ggg gat ttt gat gaa aaa aga aaa att tat gga ggc aaa gac acg agc 672
 Gly Asp Phe Asp Glu Lys Arg Lys Ile Tyr Gly Gly Lys Asp Thr Ser
 210 215 220
 aaa gtg att agc tgt tat gac atc act aaa gaa ttg tat agc aat tat 720
 Lys Val Ile Ser Cys Tyr Asp Ile Thr Lys Glu Leu Tyr Ser Asn Tyr
 225 230 235 240
 agg aag tgg aat gag aag tcc ctc caa gag cga tac aaa tct ttg tat 768
 Arg Lys Trp Asn Glu Lys Ser Leu Gln Glu Arg Tyr Lys Ser Leu Tyr
 245 250 255
 aac act atc acg cct gtt tta cac ata gag ggg caa gaa gat gat ttt 816
 Asn Thr Ile Thr Pro Val Leu His Ile Glu Gly Gln Glu Asp Asp Phe
 260 265 270
 gaa gat gat ttt gat cta gaa
 Glu Asp Asp Phe Asp Leu Glu
 275

<210> 152

<211> 279

<212> PRT

<213> Helicobacter pylori

<400> 152

Asp Ser Lys Lys Asp Ala Cys Gly Phe Ile Tyr Glu Ile Ser Glu Phe
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 Met Lys Ala Tyr Thr Ala Leu Leu Lys Lys Gln Asp Arg Tyr Val Tyr
 20 25 30
 Leu Leu Arg Tyr Leu Pro Ser Arg Tyr Trp Ala Ser Ile Leu Thr Thr
 35 40 45
 Ala Leu Tyr Val Lys Tyr Pro Asp Phe Asp Ala Leu Lys Lys Leu Leu
 50 55 60
 Val Ser Tyr Tyr Tyr Gln Thr Trp Ile Ala Gly Gly Thr Ile Thr Arg
 65 70 75 80
 Ile Lys Gln Thr Ser Ile Asn Ile Ile Lys Asn Val Lys Ser Asn Lys
 85 90 95
 Ser Val Glu Thr Ile Lys Glu Leu Ile Leu Asn Ser Ile Asp Ser Tyr
 100 105 110
 Asn Thr Phe Asp Gln Tyr Leu Tyr Asn Leu Trp Asp Ser Ser Ser Val
 115 120 125
 Tyr His Ser Lys Trp Val Arg Pro Val Leu Ala Leu Ala Asn Tyr Phe
 130 135 140
 Met Ala Asp Glu Glu Lys Pro His Phe Ile Ala Met Asp Ala Glu Thr
 145 150 155 160
 Gln Val Glu His Ile Leu Pro Gln Thr Pro Lys Arg Gly Ser Gln Trp

165 170 175
 Asn Ala Asp Phe Asp Lys Glu Lys Arg Glu Glu Trp Val Asn Asn Ile
 180 185 190
 Ala Asn Leu Thr Leu Leu Lys Arg Lys Lys Asn Ala His Ala Leu Asn
 195 200 205
 Gly Asp Phe Asp Glu Lys Arg Lys Ile Tyr Gly Gly Lys Asp Thr Ser
 210 215 220
 Lys Val Ile Ser Cys Tyr Asp Ile Thr Lys Glu Leu Tyr Ser Asn Tyr
 225 230 235 240
 Arg Lys Trp Asn Glu Lys Ser Leu Gln Glu Arg Tyr Lys Ser Leu Tyr
 245 250 255
 Asn Thr Ile Thr Pro Val Leu His Ile Glu Gly Gln Glu Asp Asp Phe
 260 265 270
 Glu Asp Asp Phe Asp Leu Glu
 275
 <210> 153
 <211> 684
 <212> DNA
 <213> Helicobacter pylori
 <220>
 <221> CDS
 <222> (1)..(684)
 <400> 153
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 Leu Met Leu His Tyr Ala Gly Glu Leu Ala Lys Lys Arg Lys Glu Lys
 1 5 10 15
 ggc att aag ctt aac tat gta gaa gcg gta gct ttg att agt gcc cat 96
 Gly Ile Lys Leu Asn Tyr Val Glu Ala Val Ala Leu Ile Ser Ala His
 20 25 30
 att atg gaa gaa gcg aga gct ggt aaa aag act gcg gct gaa ttg atg 144
 Ile Met Glu Glu Ala Arg Ala Gly Lys Lys Thr Ala Ala Glu Leu Met
 35 40 45
 caa gaa ggg cgc act ctt tta aaa ccg gat gat gtg atg gat ggc gtg 192
 Gln Glu Gly Arg Thr Leu Leu Lys Pro Asp Asp Val Met Asp Gly Val
 50 55 60
 gca agc atg atc cat gaa gtg ggt att gaa gcg atg ttt cct gat ggg 240
 Ala Ser Met Ile His Glu Val Gly Ile Glu Ala Met Phe Pro Asp Gly
 65 70 75 80
 aca aaa ctc gta acc gtg cat acc cct att gag gcc aat ggt aaa tta 288
 Thr Lys Leu Val Thr Val His Thr Pro Ile Glu Ala Asn Gly Lys Leu
 85 90 95
 gtt cct ggt gag ttg ttc tta aaa aat gaa gac atc act atc aac gaa 336
 Val Pro Gly Glu Leu Phe Leu Lys Asn Glu Asp Ile Thr Ile Asn Glu
 100 105 110
 ggc aaa aaa gcc gtt agc gtg aaa gtt aaa aat gtt ggc gac aga ccg 384
 Gly Lys Lys Ala Val Ser Val Lys Val Lys Asn Val Gly Asp Arg Pro
 115 120 125
 gtt caa atc ggc tca cac ttc cat ttc ttt gaa gtg aat aga tgc tta 432
 Val Gln Ile Gly Ser His Phe His Phe Phe Glu Val Asn Arg Cys Leu
 130 135 140
 gac ttt gac aga gaa aaa act ttc ggt aaa cgc tta gac att gcg agc 480
 Asp Phe Asp Arg Glu Lys Thr Phe Gly Lys Arg Leu Asp Ile Ala Ser
 145 150 155 160
 ggg aca gcg gta agg ttt gag cct ggc gaa gaa aaa tcc gta gaa ttg 528
 Gly Thr Ala Val Arg Phe Glu Pro Gly Glu Glu Lys Ser Val Glu Leu
 165 170 175
 att gac att ggc ggt aac aga aga atc ttt gga ttt aac gcg ttg gtt 576
 Ile Asp Ile Gly Gly Asn Arg Arg Ile Phe Gly Phe Asn Ala Leu Val
 180 185 190
 gat agg caa gca gac aac gaa agc aaa aaa att gct tta cac aga gct 624
 Asp Arg Gln Ala Asp Asn Glu Ser Lys Lys Ile Ala Leu His Arg Ala

195 200 205
 aaa gag cgt ggt ttt cat ggc gct aaa agc gat gac aac tat gta aaa 672
 Lys Glu Arg Gly Phe His Gly Ala Lys Ser Asp Asp Asn Tyr Val Lys
 210 215 220
 aca att aag gag 684
 Thr Ile Lys Glu
 225
 <210> 154
 <211> 228
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 <213> *Helicobacter pylori*
 <400> 154
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 Gly Ile Lys Leu Asn Tyr Val Glu Ala Val Ala Leu Ile Ser Ala His
 20 25 30
 Ile Met Glu Glu Ala Arg Ala Gly Lys Lys Thr Ala Ala Glu Leu Met
 35 40 45
 Gln Glu Gly Arg Thr Leu Leu Lys Pro Asp Asp Val Met Asp Gly Val
 50 55 60
 Ala Ser Met Ile His Glu Val Gly Ile Glu Ala Met Phe Pro Asp Gly
 65 70 75 80
 Thr Lys Leu Val Thr Val His Thr Pro Ile Glu Ala Asn Gly Lys Leu
 85 90 95
 Val Pro Gly Glu Leu Phe Leu Lys Asn Glu Asp Ile Thr Ile Asn Glu
 100 105 110
 Gly Lys Lys Ala Val Ser Val Lys Val Lys Asn Val Gly Asp Arg Pro
 115 120 125
 Val Gln Ile Gly Ser His Phe His Phe Phe Glu Val Asn Arg Cys Leu
 130 135 140
 Asp Phe Asp Arg Glu Lys Thr Phe Gly Lys Arg Leu Asp Ile Ala Ser
 145 150 155 160
 Gly Thr Ala Val Arg Phe Glu Pro Gly Glu Glu Lys Ser Val Glu Leu
 165 170 175
 Ile Asp Ile Gly Glu Asn Arg Arg Ile Phe Gly Phe Asn Ala Leu Val
 180 185 190
 Asp Arg Gln Ala Asp Asn Glu Ser Lys Lys Ile Ala Leu His Arg Ala
 195 200 205
 Lys Glu Arg Gly Phe His Gly Ala Lys Ser Asp Asp Asn Tyr Val Lys
 210 215 220
 Thr Ile Lys Glu
 225
 <210> 155
 <211> 486
 <212> DNA
 <213> *Helicobacter pylori*
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 <221> CDS
 <222> (1)..(486)
 <400> 155
 tta gaa gag caa aag gat aaa tct tac aag gtt gtt gaa gaa tac ccc 48
 Leu Glu Glu Gln Lys Asp Lys Ser Tyr Lys Val Val Glu Glu Tyr Pro
 1 5 10 15
 agc tca aga acc cac att ata gtg cgc gat ttg caa ggc aat gaa cgc 96
 Ser Ser Arg Thr His Ile Ile Val Arg Asp Leu Gln Gly Asn Glu Arg
 20 25 30
 gtg tta agc aat gaa gag att caa aag ctc atc aaa gaa gaa gaa gct 144
 Val Leu Ser Asn Glu Glu Ile Glu Lys Leu Ile Lys Glu Glu Glu Ala
 35 40 45
 aaa att gat aac ggc acg agc aag ctt gtc cag cct aat aat gga ggg 192
 Lys Ile Asp Asn Gly Thr Ser Lys Leu Val Gln Pro Asn Asn Gly Gly

50 55 60
 agt aat gaa ggc tca ggc ttt ggc ttg ggg agc gcg att tta ggg agc 240
 Ser Asn Glu Gly Ser Gly Phe Gly Leu Gly Ser Ala Ile Leu Gly Ser
 65 70 75 80
 gcg gcg ggg gcg att tta ggg agt tat att ggt aat aag ctt ttc aat 288
 Ala Ala Gly Ala Ile Leu Gly Ser Tyr Ile Gly Asn Lys Leu Phe Asn
 85 90 95
 aac cct aat tac cag caa aac gcc caa cgg acc tac aaa tcc cca caa 336
 Asn Pro Asn Tyr Gln Gln Asn Ala Gln Arg Thr Tyr Lys Ser Pro Gln
 100 105 110
 gct tac caa cgc tct caa aat tcc ttt tct aaa agt gcg ccc agt gct 384
 Ala Tyr Gln Arg Ser Gln Asn Ser Phe Ser Lys Ser Ala Pro Ser Ala
 115 120 125
 tca agc atg ggc gga gcg agt aag gga cag agc ggg ttt ttt ggc tct 432
 Ser Ser Met Gly Gly Ala Ser Lys Gly Gln Ser Gly Phe Phe Gly Ser
 130 135 140
 agt agg cct act agt tca ccg gcg gta agc tct ggg aca agg ggc ttt 480
 Ser Arg Pro Thr Ser Ser Pro Ala Val Ser Ser Gly Thr Arg Gly Phe
 145 150 155 160
 aac tca 486
 Asn Ser
 <210> 156
 <211> 162
 <212> PRT
 <213> Helicobacter pylori
 <400> 156
 Leu Glu Glu Gln Lys Asp Lys Ser Tyr Lys Val Val Glu Glu Tyr Pro
 1 5 10 15
 Ser Ser Arg Thr His Ile Ile Val Arg Asp Leu Gln Gly Asn Glu Arg
 20 25 30
 Val Leu Ser Asn Glu Glu Ile Gln Lys Leu Ile Lys Glu Glu Ala
 35 40 45
 Lys Ile Asp Asn Gly Thr Ser Lys Leu Val Gln Pro Asn Asn Gly Gly
 50 55 60
 Ser Asn Glu Gly Ser Gly Phe Gly Leu Gly Ser Ala Ile Leu Gly Ser
 65 70 75 80
 Ala Ala Gly Ala Ile Leu Gly Ser Tyr Ile Gly Asn Lys Leu Phe Asn
 85 90 95
 Asn Pro Asn Tyr Gln Gln Asn Ala Gln Arg Thr Tyr Lys Ser Pro Gln
 100 105 110
 Ala Tyr Gln Arg Ser Gln Asn Ser Phe Ser Lys Ser Ala Pro Ser Ala
 115 120 125
 Ser Ser Met Gly Gly Ala Ser Lys Gly Gln Ser Gly Phe Phe Gly Ser
 130 135 140
 Ser Arg Pro Thr Ser Ser Pro Ala Val Ser Ser Gly Thr Arg Gly Phe
 145 150 155 160
 Asn Ser
 <210> 157
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 <213> Helicobacter pylori
 <220>
 <221> CDS
 <222> (1)..(1032)
 <400> 157
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 Thr Phe Leu Gln Val Arg Val Gln Gly Glu Val Ser Asn Leu Thr Ile
 1 5 10 15
 cat aag gtg agc ggc cat gcg tat ttt tcg ctc aaa gac agc cag tcg 96
 His Lys Val Ser Gly His Ala Tyr Phe Ser Leu Lys Asp Ser Gln Ser
 20 25 30

gtt att aaa tgc gtg ctg ttt aaa ggg aac gct aac agg ctc aaa ttc 144
 Val Ile Lys Cys Val Leu Phe Lys Gly Asn Ala Asn Arg Leu Lys Phe
 35 40 45
 gct tta aaa gaa ggg cag gaa gtg gtt gtt ttt ggg ggt att agc gtg 192
 Ala Leu Lys Glu Gly Gln Glu Val Val Val Phe Gly Gly Ile Ser Val
 50 55 60
 tat gtc cca agg ggg gat tat caa atc aat tgc ttt gaa ata gag cct 240
 Tyr Val Pro Arg Gly Asp Tyr Gln Ile Asn Cys Phe Glu Ile Glu Pro
 65 70 75 80
 aag gat ata ggt tca tta act tta gct tta gag caa ttg aaa gaa aaa 288
 Lys Asp Ile Gly Ser Leu Thr Leu Ala Leu Glu Gln Leu Lys Glu Lys
 85 90 95
 tta cgc ctt aaa ggc tat ttt gat gaa gaa aat aaa tta ccc aaa ccg 336
 Leu Arg Leu Lys Gly Tyr Phe Asp Glu Glu Asn Lys Leu Pro Lys Pro
 100 105 110
 cat ttt cct aaa cga gtg gca gtc atc act tct caa aat tca gcc gct 384
 His Phe Pro Lys Arg Val Ala Val Ile Thr Ser Gln Asn Ser Ala Ala
 115 120 125
 tgg gcg gac atg aaa aag atc gct tcc aaa cga tgg ccg atg tgt gaa 432
 Trp Ala Asp Met Lys Lys Ile Ala Ser Lys Arg Trp Pro Met Cys Glu
 130 135 140
 tta gtt tgt atc aac acc tta atg caa ggg gag ggc tgc gtt caa agc 480
 Leu Val Cys Ile Asn Thr Leu Met Gln Gly Glu Gly Cys Val Gln Ser
 145 150 155 160
 gtg gtg gaa agc atc gtt tat gcg gat agt ttt cat gac aca aaa aac 528
 Val Val Glu Ser Ile Val Tyr Ala Asp Ser Phe His Asp Thr Lys Asn
 165 170 175
 gct ttt gat gcg att gta gtg gct agg ggt ggg ggg agc atg gag gat 576
 Ala Phe Asp Ala Ile Val Val Ala Arg Gly Gly Gly Ser Met Glu Asp
 180 185 190
 ttg tat tct ttc aat gat gaa aaa atc gct gat gct ctg tat ttg gcc 624
 Leu Tyr Ser Phe Asn Asp Glu Lys Ile Ala Asp Ala Leu Tyr Leu Ala
 195 200 205
 aaa acc ttc agc atg tca gct att ggg cat gag agc gat ttt tta ttg 672
 Lys Thr Phe Ser Met Ser Ala Ile Gly His Glu Ser Asp Phe Leu Leu
 210 215 220
 agc gat tta gtg gcg gat tta agg gct tct acg cct tca aac gcg atg 720
 Ser Asp Leu Val Ala Asp Leu Arg Ala Ser Thr Pro Ser Asn Ala Met
 225 230 235 240
 gaa att tta ctc ccc agc agc gat gaa tgg ttg caa aga ctt gat ggg 768
 Glu Ile Leu Leu Pro Ser Ser Asp Glu Trp Leu Gln Arg Leu Asp Gly
 245 250 255
 ttt aat gtg aaa ttg cac cgc tcg ttt aaa act ttg ctc cac caa aaa 816
 Phe Asn Val Lys Leu His Arg Ser Phe Lys Thr Leu Leu His Gln Lys
 260 265 270
 aag gcg cat tta gag cat tta gtg gct tct tta aaa cga ttg agt ttt 864
 Lys Ala His Leu Glu His Leu Val Ala Ser Leu Lys Arg Leu Ser Phe
 275 280 285
 gaa aac aag cac cat tta aac gct tta aaa cta gaa aaa tta aaa atc 912
 Glu Asn Lys His His Leu Asn Ala Leu Lys Leu Glu Lys Leu Lys Ile
 290 295 300
 gcc cta gaa aat aaa act cta gaa ttt tta cgc ttt aaa aaa acg ctt 960
 Ala Leu Glu Asn Lys Thr Leu Glu Phe Leu Arg Phe Lys Lys Thr Leu
 305 310 315 320
 tta gaa aaa atc tct act caa aca tta aca agc cct ttt tta caa act 1008
 Leu Glu Lys Ile Ser Thr Gln Thr Leu Thr Ser Pro Phe Leu Gln Thr
 325 330 335
 aaa aca gag cga ttg aac agg cta 1032
 Lys Thr Glu Arg Leu Asn Arg Leu
 340

<210> 158

<211> 344

<212> PRT

<213> Helicobacter pylori

<400> 158

Thr Phe Leu Gln Val Arg Val Gln Gly Glu Val Ser Asn Leu Thr Ile
 1 5 10 15
 His Lys Val Ser Gly His Ala Tyr Phe Ser Leu Lys Asp Ser Gln Ser
 20 25 30
 Val Ile Lys Cys Val Leu Phe Lys Gly Asn Ala Asn Arg Leu Lys Phe
 35 40 45
 Ala Leu Lys Glu Gly Gln Glu Val Val Phe Gly Gly Ile Ser Val
 50 55 60
 Tyr Val Pro Arg Gly Asp Tyr Gln Ile Asn Cys Phe Glu Ile Glu Pro
 65 70 75 80
 Lys Asp Ile Gly Ser Leu Thr Leu Ala Leu Glu Gln Leu Lys Glu Lys
 85 90 95
 Leu Arg Leu Lys Gly Tyr Phe Asp Glu Glu Asn Lys Leu Pro Lys Pro
 100 105 110
 His Phe Pro Lys Arg Val Ala Val Ile Thr Ser Gln Asn Ser Ala Ala
 115 120 125
 Trp Ala Asp Met Lys Lys Ile Ala Ser Lys Arg Trp Pro Met Cys Glu
 130 135 140
 Leu Val Cys Ile Asn Thr Leu Met Gln Gly Glu Gly Cys Val Gln Ser
 145 150 155 160
 Val Val Glu Ser Ile Val Tyr Ala Asp Ser Phe His Asp Thr Lys Asn
 165 170 175
 Ala Phe Asp Ala Ile Val Val Ala Arg Gly Gly Gly Ser Met Glu Asp
 180 185 190
 Leu Tyr Ser Phe Asn Asp Glu Lys Ile Ala Asp Ala Leu Tyr Leu Ala
 195 200 205
 Lys Thr Phe Ser Met Ser Ala Ile Gly His Glu Ser Asp Phe Leu Leu
 210 215 220
 Ser Asp Leu Val Ala Asp Leu Arg Ala Ser Thr Pro Ser Asn Ala Met
 225 230 235 240
 Glu Ile Leu Leu Pro Ser Ser Asp Glu Trp Leu Gln Arg Leu Asp Gly
 245 250 255
 Phe Asn Val Lys Leu His Arg Ser Phe Lys Thr Leu Leu His Gln Lys
 260 265 270
 Lys Ala His Leu Glu His Leu Val Ala Ser Leu Lys Arg Leu Ser Phe
 275 280 285
 Glu Asn Lys His His Leu Asn Ala Leu Lys Leu Glu Lys Leu Lys Ile
 290 295 300
 Ala Leu Glu Asn Lys Thr Leu Glu Phe Leu Arg Phe Lys Lys Thr Leu
 305 310 315 320
 Leu Glu Lys Ile Ser Thr Gln Thr Leu Thr Ser Pro Phe Leu Gln Thr
 325 330 335
 Lys Thr Glu Arg Leu Asn Arg Leu
 340

<210> 159

<211> 363

<212> DNA

<213> Helicobacter pylori

<220>

<221> CDS

<222> (1)..(363)

<400> 159

atc atc aaa ggc ggg ttc att gcg ttg agt caa atg ggt gac gcg aac 48
 Ile Ile Lys Gly Gly Phe Ile Ala Leu Ser Gln Met Gly Asp Ala Asn
 1 5 10 15
 gct tct atc cct acc cca caa cca gtt tat tac aga gaa atg ttc gct 96
 Ala Ser Ile Pro Thr Pro Gln Pro Val Tyr Tyr Arg Glu Met Phe Ala

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      20      25      30
cat cat ggt aaa gcc aaa tac gat gca aac atc act ttt gtg tct caa 144
His His Gly Lys Ala Lys Tyr Asp Ala Asn Ile Thr Phe Val Ser Gln
      35      40      45
gcg gct tat gac aaa ggc att aaa gaa gaa tta ggg ctt gaa aga caa 192
Ala Ala Tyr Asp Lys Gly Ile Lys Glu Glu Leu Gly Leu Glu Arg Gln
      50      55      60
gtg ttg ccg gta aaa aat tgc aga aac atc act aaa gac atg caa 240
Val Leu Pro Val Lys Asn Cys Arg Asn Ile Thr Lys Lys Asp Met Gln
      65      70      75      80
ttc aac gac act acc gct cac att gaa gtc aat cct gaa act tac cat 288
Phe Asn Asp Thr Thr Ala His Ile Glu Val Asn Pro Glu Thr Tyr His
      85      90      95
gtg ttc gtg gat ggc aaa gaa gta act tct aaa cca gcc aat aaa gtg 336
Val Phe Val Asp Gly Lys Glu Val Thr Ser Lys Pro Ala Asn Lys Val
      100      105      110
agc ttg gcg caa ctc ttt agc att ttc 363
Ser Leu Ala Gln Leu Phe Ser Ile Phe
      115      120
<210> 160
<211> 121
<212> PRT
<213> Helicobacter pylori
<400> 160
Ile Ile Lys Gly Gly Phe Ile Ala Leu Ser Gln Met Gly Asp Ala Asn
  1      5      10      15
Ala Ser Ile Pro Thr Pro Gln Pro Val Tyr Tyr Arg Glu Met Phe Ala
      20      25      30
His His Gly Lys Ala Lys Tyr Asp Ala Asn Ile Thr Phe Val Ser Gln
      35      40      45
Ala Ala Tyr Asp Lys Gly Ile Lys Glu Glu Leu Gly Leu Glu Arg Gln
      50      55      60
Val Leu Pro Val Lys Asn Cys Arg Asn Ile Thr Lys Lys Asp Met Gln
      65      70      75      80
Phe Asn Asp Thr Thr Ala His Ile Glu Val Asn Pro Glu Thr Tyr His
      85      90      95
Val Phe Val Asp Gly Lys Glu Val Thr Ser Lys Pro Ala Asn Lys Val
      100      105      110
Ser Leu Ala Gln Leu Phe Ser Ile Phe
      115      120
<210> 161
<211> 717
<212> DNA
<213> Helicobacter pylori
<220>
<221> CDS
<222> (1)..(717)
<400> 161
cgg act aat aaa gcc ttg tat caa ttc att ttg aga ata gct caa aaa 48
Arg Thr Asn Lys Ala Leu Tyr Gln Phe Ile Leu Arg Ile Ala Gln Lys
  1      5      10      15
gac aat ttt gct tca gcg tat cta aca gtc aaa tta gaa tac cca caa 96
Asp Asn Phe Ala Ser Ala Tyr Leu Thr Val Lys Leu Glu Tyr Pro Gln
      20      25      30
aga cac gaa gtc tct agc gtt att gaa gag gag tta aaa aag aga gaa 144
Arg His Glu Val Ser Ser Val Ile Glu Glu Glu Leu Lys Lys Arg Glu
      35      40      45
gaa gca aag agg cag aaa gaa ttg att aag caa gaa aat ctt aac acc 192
Glu Ala Lys Arg Gln Lys Glu Leu Ile Lys Gln Glu Asn Leu Asn Thr
      50      55      60
aca gcc tac atc aat aga gtg atg atg gcg agc aat gaa cag att atc 240

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Thr Ala Tyr Ile Asn Arg Val Met Met Ala Ser Asn Glu Gln Ile Ile
 65 70 75 80
 aac aaa gaa aaa ata aga gaa gaa aag caa aaa att atc tta gat caa 288
 Asn Lys Glu Lys Ile Arg Glu Glu Lys Gln Lys Ile Ile Leu Asp Gln
 85 90 95
 gca aag gcg cta gag act caa tat gtg cat aat gcc tta aaa aga aac 336
 Ala Lys Ala Leu Glu Thr Gln Tyr Val His Asn Ala Leu Lys Arg Asn
 100 105 110
 ccc gtg cct aga aac tac aac tac tac caa gcg cct gaa aaa cgc tct 384
 Pro Val Pro Arg Asn Tyr Asn Tyr Tyr Gln Ala Pro Glu Lys Arg Ser
 115 120 125
 aaa cat att atg ccc tct gaa att ttt gat gat ggc aca ttc act tat 432
 Lys His Ile Met Pro Ser Glu Ile Phe Asp Asp Gly Thr Phe Thr Tyr
 130 135 140
 ttt ggt ttc aaa aac atc act ctc caa cct gct att ttt gtg gtt caa 480
 Phe Gly Phe Lys Asn Ile Thr Leu Gln Pro Ala Ile Phe Val Val Gln
 145 150 155 160
 cct gat ggg aaa ttg agc atg act gat gcc gcc att gat cct aac atg 528
 Pro Asp Gly Lys Leu Ser Met Thr Asp Ala Ala Ile Asp Pro Asn Met
 165 170 175
 acc aat tca gga ttg aga tgg tat aga gtt aat gaa att gca gaa aaa 576
 Thr Asn Ser Gly Leu Arg Trp Tyr Arg Val Asn Glu Ile Ala Glu Lys
 180 185 190
 ttt aag ctc att aaa gac aaa gcc ctt gta aca gta atc aat aaa ggc 624
 Phe Lys Leu Ile Lys Asp Lys Ala Leu Val Thr Val Ile Asn Lys Gly
 195 200 205
 tat ggg aaa aat cca ttg aca aaa aat tac aat atc aaa aac tat ggt 672
 Tyr Gly Lys Asn Pro Leu Thr Lys Asn Tyr Asn Ile Lys Asn Tyr Gly
 210 215 220
 gaa ttg gag cgt gtg att aaa aag ctc cct ctt gtc aga gat aaa 717
 Glu Leu Glu Arg Val Ile Lys Lys Leu Pro Leu Val Arg Asp Lys
 225 230 235
 <210> 162
 <211> 239
 <212> PRT
 <213> *Helicobacter pylori*
 <400> 162
 Arg Thr Asn Lys Ala Leu Tyr Gln Phe Ile Leu Arg Ile Ala Gln Lys
 1 5 10 15
 Asp Asn Phe Ala Ser Ala Tyr Leu Thr Val Lys Leu Glu Tyr Pro Gln
 20 25 30
 Arg His Glu Val Ser Ser Val Ile Glu Glu Glu Leu Lys Lys Arg Glu
 35 40 45
 Glu Ala Lys Arg Gln Lys Glu Leu Ile Lys Gln Glu Asn Leu Asn Thr
 50 55 60
 Thr Ala Tyr Ile Asn Arg Val Met Met Ala Ser Asn Glu Gln Ile Ile
 65 70 75 80
 Asn Lys Glu Lys Ile Arg Glu Glu Lys Gln Lys Ile Ile Leu Asp Gln
 85 90 95
 Ala Lys Ala Leu Glu Thr Gln Tyr Val His Asn Ala Leu Lys Arg Asn
 100 105 110
 Pro Val Pro Arg Asn Tyr Asn Tyr Tyr Gln Ala Pro Glu Lys Arg Ser
 115 120 125
 Lys His Ile Met Pro Ser Glu Ile Phe Asp Asp Gly Thr Phe Thr Tyr
 130 135 140
 Phe Gly Phe Lys Asn Ile Thr Leu Gln Pro Ala Ile Phe Val Val Gln
 145 150 155 160
 Pro Asp Gly Lys Leu Ser Met Thr Asp Ala Ala Ile Asp Pro Asn Met
 165 170 175
 Thr Asn Ser Gly Leu Arg Trp Tyr Arg Val Asn Glu Ile Ala Glu Lys
 180 185 190

Phe Lys Leu Ile Lys Asp Lys Ala Leu Val Thr Val Ile Asn Lys Gly
 195 200 205
 Tyr Gly Lys Asn Pro Leu Thr Lys Asn Tyr Asn Ile Lys Asn Tyr Gly
 210 215 220
 Glu Leu Glu Arg Val Ile Lys Lys Leu Pro Leu Val Arg Asp Lys
 225 230 235
 <210> 163
 <211> 1077
 <212> DNA
 <213> *Helicobacter pylori*
 <220>
 <221> CDS
 <222> (1)..(1077)
 <400> 163
 gaa ggc act aaa gag ctt ggt gcg gtg ggg ttt gcg caa ctt tta gag 48
 Glu Gly Thr Lys Glu Leu Gly Ala Val Phe Ala Gln Leu Leu Glu
 1 5 10 15
 caa aaa gcg atc agt ttg aat gtg gat acc agc aca gaa gat ttg caa 96
 Gln Lys Ala Ile Ser Leu Asn Val Asp Thr Ser Thr Glu Asp Leu Gln
 20 25 30
 atc act tta gaa ttt tta aaa gaa tac gaa gat gaa gcc att acg cgc 144
 Ile Thr Leu Glu Phe Leu Lys Glu Tyr Glu Asp Glu Ala Ile Thr Arg
 35 40 45
 tta aaa gag ctt tta aaa tcc cct aat ttc acg caa aac gct tta gaa 192
 Leu Lys Glu Leu Leu Lys Ser Pro Asn Phe Thr Gln Asn Ala Leu Glu
 50 55 60
 aaa gtc aaa acc caa atg tta gcc gca ctt tta caa aaa gaa agc gat 240
 Lys Val Lys Thr Gln Met Leu Ala Ala Leu Leu Gln Lys Glu Ser Asp
 65 70 75 80
 ttt gac tat ttg gct aaa ttg act tta aag caa gag ctt ttt gct aac 288
 Phe Asp Tyr Leu Ala Lys Leu Thr Leu Lys Gln Glu Leu Phe Ala Asn
 85 90 95
 acc cct tta gct aac gca gcc tta ggc act aaa gag agc att caa aaa 336
 Thr Pro Leu Ala Asn Ala Ala Leu Gly Thr Lys Glu Ser Ile Gln Lys
 100 105 110
 atc aag cta gac gat ttg aaa cag caa ttt gct aag gtc ttt gaa ctc 384
 Ile Lys Leu Asp Asp Leu Lys Gln Phe Ala Lys Val Phe Glu Leu
 115 120 125
 aat aag ctc gtg gtg gtg ctt ggg ggc gat ttg aaa atc gat caa acc 432
 Asn Lys Leu Val Val Val Leu Gly Gly Asp Leu Lys Ile Asp Gln Thr
 130 135 140
 ctt aag cgt ttg aat aac gcc ctt aat ttc ttg cca caa ggt aaa gcg 480
 Leu Lys Arg Leu Asn Asn Ala Leu Asn Phe Leu Pro Gln Gly Lys Ala
 145 150 155 160
 tat gaa gag cct tat ttt gaa acg agc gat aaa aaa agc gaa aaa gtc 528
 Tyr Glu Glu Pro Tyr Phe Glu Thr Ser Asp Lys Lys Ser Glu Lys Val
 165 170 175
 ctc tat aaa gac act gag cag gct ttc gtg tat ttt ggt gcg ccc ttt 576
 Leu Tyr Lys Asp Thr Glu Gln Ala Phe Val Tyr Phe Gly Ala Pro Phe
 180 185 190
 aaa atc aag gat tta aaa cag gat tta gcg aaa tct aaa gtc atg atg 624
 Lys Ile Lys Asp Leu Lys Gln Asp Leu Ala Lys Ser Lys Val Met Met
 195 200 205
 ttt gtg ctt ggt ggg ggg ttt ggc tct cgt tta atg gaa aaa atc agg 672
 Phe Val Leu Gly Gly Gly Phe Gly Ser Arg Leu Met Glu Lys Ile Arg
 210 215 220
 gtt caa gag gga tta gct tat agc gtg tat atc cgc tcc aat ttt tct 720
 Val Gln Glu Gly Leu Ala Tyr Ser Val Tyr Ile Arg Ser Asn Phe Ser
 225 230 235 240
 aaa gtg gcg cat ttt gcg agc ggg tat ttg caa acc aag ctc agc act 768
 Lys Val Ala His Phe Ala Ser Gly Tyr Leu Gln Thr Lys Leu Ser Thr

245 250 255
 caa act aaa agc gtt gcc tta gtt aaa aaa atc gtt aag gaa ttt ata 816
 Gln Thr Lys Ser Val Ala Leu Val Lys Lys Ile Val Lys Glu Phe Ile
 260 265 270
 gaa aaa ggc atg acg caa caa gaa tta gac gac gct aaa aag ttt tta 864
 Glu Lys Gly Met Thr Gln Gln Glu Leu Asp Asp Ala Lys Lys Phe Leu
 275 280 285
 cta ggc tct gag cct tta agg aat gaa acg atc tct agc cgc ttg aac 912
 Leu Gly Ser Glu Pro Leu Arg Asn Glu Thr Ile Ser Ser Arg Leu Asn
 290 295 300
 acc act tac aat tat ttt tat tta ggt ttg cct tta aat ttt aac caa 960
 Thr Thr Tyr Asn Tyr Phe Tyr Leu Gly Leu Pro Leu Asn Phe Asn Gln
 305 310 315 320
 acg ctg ctc aat caa atc caa aaa atg agt ttg aaa gaa atc aat gat 1008
 Thr Leu Leu Asn Gln Ile Gln Lys Met Ser Leu Lys Glu Ile Asn Asp
 325 330 335
 ttc att aaa gcc cac acc gaa atc aac gac ttg act ttt gct att gtg 1056
 Phe Ile Lys Ala His Thr Glu Ile Asn Asp Leu Thr Phe Ala Ile Val
 340 345 350
 agc aat aaa aag aag gac aaa 1077
 Ser Asn Lys Lys Lys Asp Lys
 355
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 <211> 359
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 <213> Helicobacter pylori
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 Glu Gly Thr Lys Glu Leu Gly Ala Val Gly Phe Ala Gln Leu Leu Glu
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 Gln Lys Ala Ile Ser Leu Asn Val Asp Thr Ser Thr Glu Asp Leu Gln
 20 25 30
 Ile Thr Leu Glu Phe Leu Lys Glu Tyr Glu Asp Glu Ala Ile Thr Arg
 35 40 45
 Leu Lys Glu Leu Leu Lys Ser Pro Asn Phe Thr Gln Asn Ala Leu Glu
 50 55 60
 Lys Val Lys Thr Gln Met Leu Ala Ala Leu Leu Gln Lys Glu Ser Asp
 65 70 75 80
 Phe Asp Tyr Leu Ala Lys Leu Thr Leu Lys Gln Glu Leu Phe Ala Asn
 85 90 95
 Thr Pro Leu Ala Asn Ala Ala Leu Gly Thr Lys Glu Ser Ile Gln Lys
 100 105 110
 Ile Lys Leu Asp Asp Leu Lys Gln Gln Phe Ala Lys Val Phe Glu Leu
 115 120 125
 Asn Lys Leu Val Val Val Leu Gly Gly Asp Leu Lys Ile Asp Gln Thr
 130 135 140
 Leu Lys Arg Leu Asn Asn Ala Leu Asn Phe Leu Pro Gln Gly Lys Ala
 145 150 155 160
 Tyr Glu Glu Pro Tyr Phe Glu Thr Ser Asp Lys Lys Ser Glu Lys Val
 165 170 175
 Leu Tyr Lys Asp Thr Glu Gln Ala Phe Val Tyr Phe Gly Ala Pro Phe
 180 185 190
 Lys Ile Lys Asp Leu Lys Gln Asp Leu Ala Lys Ser Lys Val Met Met
 195 200 205
 Phe Val Leu Gly Gly Gly Phe Gly Ser Arg Leu Met Glu Lys Ile Arg
 210 215 220
 Val Gln Glu Gly Leu Ala Tyr Ser Val Tyr Ile Arg Ser Asn Phe Ser
 225 230 235 240
 Lys Val Ala His Phe Ala Ser Gly Tyr Leu Gln Thr Lys Leu Ser Thr
 245 250 255
 Gln Thr Lys Ser Val Ala Leu Val Lys Lys Ile Val Lys Glu Phe Ile
 260 265 270

Glu Lys Gly Met Thr Gln Gln Glu Leu Asp Asp Ala Lys Lys Phe Leu
 275 280 285
 Leu Gly Ser Glu Pro Leu Arg Asn Glu Thr Ile Ser Ser Arg Leu Asn
 290 295 300
 Thr Thr Tyr Asn Tyr Phe Tyr Leu Gly Leu Pro Leu Asn Phe Asn Gln
 305 310 315 320
 Thr Leu Leu Asn Gln Ile Gln Lys Met Ser Leu Lys Glu Ile Asn Asp
 325 330 335
 Phe Ile Lys Ala His Thr Glu Ile Asn Asp Leu Thr Phe Ala Ile Val
 340 345 350
 Ser Asn Lys Lys Lys Asp Lys
 355

<210> 165

<211> 882

<212> DNA

<213> *Helicobacter pylori*

<220>

<221> CDS

<222> (1)..(882)

<400> 165

gaa gag gat ggg aat gaa agt att gcc tat gat ttt tca agc gct aag	48
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1 5 10 15	
gag ttg cta gaa ttg tgc caa aaa cac caa aaa agc atc gct gaa atc	96
Glu Leu Leu Glu Leu Cys Gln Lys His Gln Lys Ser Ile Ala Glu Ile	
20 25 30	
gtg cgt ttg aga gaa aac gcc ctg aaa aac cac cct gat gca acg atg	144
Val Arg Leu Arg Glu Asn Ala Leu Lys Asn His Pro Asp Ala Thr Met	
35 40 45	
gtt aaa att tat cat gcg atg ctt gag tgt tat gat aat ggg gct aat	192
Val Lys Ile Tyr His Ala Met Leu Glu Cys Tyr Asp Asn Gly Ala Asn	
50 55 60	
tct aaa gaa agg tat ctg cct ggt tct ttg aaa gta aca cga ttg gcc	240
Ser Lys Glu Arg Tyr Leu Pro Gly Ser Leu Lys Val Thr Arg Leu Ala	
65 70 75 80	
cca agc att aaa acg cgc cta gaa aaa cac ccc aca agc ggg aaa gac	288
Pro Ser Ile Lys Thr Arg Leu Glu Lys His Pro Thr Ser Gly Lys Asp	
85 90 95	
ccc tta gcc ttg att gat tac att tcg ctt tac gct cgc gcc att gct	336
Pro Leu Ala Leu Ile Asp Tyr Ile Ser Leu Tyr Ala Arg Ala Ile Ala	
100 105 110	
gaa gaa aac gct agc gga ggc aag gtg gta acc gcc ccc act aat ggg	384
Glu Glu Asn Ala Ser Gly Gly Lys Val Val Thr Ala Pro Thr Asn Gly	
115 120 125	
gcg tgc gcg gtg gtg cca agc gtg ctt tta tac gct aaa aac cat ttg	432
Ala Cys Ala Val Val Pro Ser Val Leu Leu Tyr Ala Lys Asn His Leu	
130 135 140	
ttt gaa aat tta tcg caa aag gct atc aat gat ttt tta ctc act agt	480
Phe Glu Asn Leu Ser Gln Lys Ala Ile Asn Asp Phe Leu Leu Thr Ser	
145 150 155 160	
gcg gcg att ggc tat ctt tac aag aaa aac gct tcc ttg agt ggc gca	528
Ala Ala Ile Gly Tyr Leu Tyr Lys Lys Asn Ala Ser Leu Ser Gly Ala	
165 170 175	
gaa gcc ggg tgt cag gct gaa att ggc gtg gca agc tct atg gct gcg	576
Glu Ala Gly Cys Gln Ala Glu Ile Gly Val Ala Ser Ser Met Ala Ala	
180 185 190	
ggg ggg tta gct cat ttg tgc caa gcg acc acg caa cag gtt ttg atc	624
Gly Gly Leu Ala His Leu Cys Gln Ala Thr Thr Gln Gln Val Leu Ile	
195 200 205	
gct agt gaa atc gct atg gaa cac cat tta gga ttg aca tgc gat ccg	672
Ala Ser Glu Ile Ala Met Glu His His Leu Gly Leu Thr Cys Asp Pro	

210 215 220
 gtg ggg ggc ttg gtg caa atc cct tgc att gaa cgc aat gtt tta ggg 720
 Val Gly Gly Leu Val Gln Ile Pro Cys Ile Glu Arg Asn Val Leu Gly
 225 230 235 240
 gcg att aaa gcg atc agc gct tct aaa cta gcc tta gaa gat gaa tac 768
 Ala Ile Lys Ala Ile Ser Ala Ser Lys Leu Ala Leu Glu Asp Glu Tyr
 245 250 255
 aag cct aaa gtg agt ctg gat gaa gtg atc gct aca atg tat gcg acc 816
 Lys Pro Lys Val Ser Leu Asp Glu Val Ile Ala Thr Met Tyr Ala Thr
 260 265 270
 gga aaa gac atg aat gaa aaa tac aaa gag act tcg tta ggg ggg tta 864
 Gly Lys Asp Met Asn Glu Lys Tyr Lys Glu Thr Ser Leu Gly Gly Leu
 275 280 285
 gcc aaa acc tta aaa tgc 882
 Ala Lys Thr Leu Lys Cys
 290
 <210> 166
 <211> 294
 <212> PRT
 <213> Helicobacter pylori
 <400> 166
 Glu Glu Asp Gly Asn Glu Ser Ile Ala Tyr Asp Phe Ser Ser Ala Lys
 1 5 10 15
 Glu Leu Leu Glu Leu Cys Gln Lys His Gln Lys Ser Ile Ala Glu Ile
 20 25 30
 Val Arg Leu Arg Glu Asn Ala Leu Lys Asn His Pro Asp Ala Thr Met
 35 40 45
 Val Lys Ile Tyr His Ala Met Leu Glu Cys Tyr Asp Asn Gly Ala Asn
 50 55 60
 Ser Lys Glu Arg Tyr Leu Pro Gly Ser Leu Lys Val Thr Arg Leu Ala
 65 70 75 80
 Pro Ser Ile Lys Thr Arg Leu Glu Lys His Pro Thr Ser Gly Lys Asp
 85 90 95
 Pro Leu Ala Leu Ile Asp Tyr Ile Ser Leu Tyr Ala Arg Ala Ile Ala
 100 105 110
 Glu Glu Asn Ala Ser Gly Gly Lys Val Val Thr Ala Pro Thr Asn Gly
 115 120 125
 Ala Cys Ala Val Val Pro Ser Val Leu Leu Tyr Ala Lys Asn His Leu
 130 135 140
 Phe Glu Asn Leu Ser Gln Lys Ala Ile Asn Asp Phe Leu Leu Thr Ser
 145 150 155 160
 Ala Ala Ile Gly Tyr Leu Tyr Lys Lys Asn Ala Ser Leu Ser Gly Ala
 165 170 175
 Glu Ala Gly Cys Gln Ala Glu Ile Gly Val Ala Ser Ser Met Ala Ala
 180 185 190
 Gly Gly Leu Ala His Leu Cys Gln Ala Thr Thr Gln Gln Val Leu Ile
 195 200 205
 Ala Ser Glu Ile Ala Met Glu His His Leu Gly Leu Thr Cys Asp Pro
 210 215 220
 Val Gly Gly Leu Val Gln Ile Pro Cys Ile Glu Arg Asn Val Leu Gly
 225 230 235 240
 Ala Ile Lys Ala Ile Ser Ala Ser Lys Leu Ala Leu Glu Asp Glu Tyr
 245 250 255
 Lys Pro Lys Val Ser Leu Asp Glu Val Ile Ala Thr Met Tyr Ala Thr
 260 265 270
 Gly Lys Asp Met Asn Glu Lys Tyr Lys Glu Thr Ser Leu Gly Gly Leu
 275 280 285
 Ala Lys Thr Leu Lys Cys
 290
 <210> 167
 <211> 177

<212> DNA

<213> Helicobacter pylori

<220>

<221> CDS

<222> (1)..(177)

<400> 167

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gag caa gcg gtt aaa atc gtg gaa aaa cgc ttg aaa aaa gag ggc atg   48
Glu Gln Ala Val Lys Ile Val Glu Lys Arg Leu Lys Lys Glu Gly Met
1           5           10           15
aaa ttg agc gat ttt aac gaa gaa gaa ttg aaa atc atg ttt gaa gcg   96
Lys Leu Ser Asp Phe Asn Glu Glu Glu Leu Lys Ile Met Phe Glu Ala
           20           25           30
gaa gag aaa agg ctt tta gaa caa atc caa act aag cat ttt aaa gaa   144
Glu Glu Lys Arg Leu Leu Glu Gln Ile Gln Thr Lys His Phe Lys Glu
           35           40           45
gtt tgg gaa aag ggc gac aat gag caa gga aaa   177
Val Trp Glu Lys Gly Asp Asn Glu Gln Gly Lys
           50           55

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<210> 168

<211> 59

<212> PRT

<213> Helicobacter pylori

<400> 168

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Glu Gln Ala Val Lys Ile Val Glu Lys Arg Leu Lys Lys Glu Gly Met
1           5           10           15
Lys Leu Ser Asp Phe Asn Glu Glu Glu Leu Lys Ile Met Phe Glu Ala
           20           25           30
Glu Glu Lys Arg Leu Leu Glu Gln Ile Gln Thr Lys His Phe Lys Glu
           35           40           45
Val Trp Glu Lys Gly Asp Asn Glu Gln Gly Lys
           50           55

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<210> 169

<211> 971

<212> DNA

<213> Helicobacter pylori

<220>

<221> CDS

<222> (1)..(969)

<400> 169

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gtt atc act aat cgt gga ggg cgc act tgc cat gcc gct att gtg gcg   48
Val Ile Thr Asn Arg Gly Gly Arg Thr Cys His Ala Ala Ile Val Ala
1           5           10           15
aga gaa att ggc gtg cca gct atc gtt ggg gtg agc ggg gcg act gat   96
Arg Glu Ile Gly Val Pro Ala Ile Val Gly Val Ser Gly Ala Thr Asp
           20           25           30
agc ctt tat acc ggc atg gaa atc acg gtt tct tgc gct gag ggc gaa   144
Ser Leu Tyr Thr Gly Met Glu Ile Thr Val Ser Cys Ala Glu Gly Glu
           35           40           45
gag ggc tat gtg tat gcg ggc att tat gag cat gaa att gaa agg gtg   192
Glu Gly Tyr Val Tyr Ala Gly Ile Tyr Glu His Glu Ile Glu Arg Val
           50           55           60
gag ctt tct aac atg caa gaa act caa aca aaa att tac atc aat att   240
Glu Leu Ser Asn Met Gln Glu Thr Gln Thr Lys Ile Tyr Ile Asn Ile
           65           70           75           80
gga aac cct gaa aaa gcc ttt ggc ttt tct caa ctc cct aat cac ggc   288
Gly Asn Pro Glu Lys Ala Phe Gly Phe Ser Gln Leu Pro Asn His Gly
           85           90           95
gta ggg cta gcc agg atg gaa atg att att tta aat caa atc aaa gcc   336
Val Gly Leu Ala Arg Met Glu Met Ile Ile Leu Asn Gln Ile Lys Ala
           100           105           110
cac cct tta gct tta gtg gat ttg cac cac aaa aaa agc gtg aaa gaa   384

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His Pro Leu Ala Leu Val Asp Leu His His Lys Lys Ser Val Lys Glu
 115 120 125
 aaa aat gaa att gaa aac ctc atg gca ggc tat gct aac cct aaa gat 432
 Lys Asn Glu Ile Glu Asn Leu Met Ala Gly Tyr Ala Asn Pro Lys Asp
 130 135 140
 ttt ttt gtg aaa aaa atc gct gaa ggc att ggc atg atc agt gca gcg 480
 Phe Phe Val Lys Lys Ile Ala Glu Gly Ile Gly Met Ile Ser Ala Ala
 145 150 155 160
 ttt tac cct aaa cct gtc att gtg aga acg agc gat ttc aaa tcc aat 528
 Phe Tyr Pro Lys Pro Val Ile Val Arg Thr Ser Asp Phe Lys Ser Asn
 165 170 175
 gaa tac atg cgc atg ctt ggc ggc tct agc tat gag cct aat gaa gaa 576
 Glu Tyr Met Arg Met Leu Gly Gly Ser Ser Tyr Glu Pro Asn Glu Glu
 180 185 190
 aac ccc atg ctt ggc tat agg ggg gct agt cgg tat tat tca gag agc 624
 Asn Pro Met Leu Gly Tyr Arg Gly Ala Ser Arg Tyr Tyr Ser Glu Ser
 195 200 205
 tat aat gaa gcg ttt tcg tgg gag tgt gaa gcc tta gcg tta gtg agg 672
 Tyr Asn Glu Ala Phe Ser Trp Glu Cys Glu Ala Leu Ala Leu Val Arg
 210 215 220
 gaa gaa atg gga tta acc aac atg aaa gtg atg atc cct ttt ttg cga 720
 Glu Glu Met Gly Leu Thr Asn Met Lys Val Met Ile Pro Phe Leu Arg
 225 230 235 240
 acc att gaa gag ggt aaa aaa gtc cta gaa atc tta aga aaa aac aat 768
 Thr Ile Glu Glu Gly Lys Lys Val Leu Glu Ile Leu Arg Lys Asn Asn
 245 250 255
 tta gaa tcc ggt aaa aac ggg ctt gaa att tat atc atg tgc gaa ttg 816
 Leu Glu Ser Gly Lys Asn Gly Leu Glu Ile Tyr Ile Met Cys Glu Leu
 260 265 270
 ccg gtg aat gtc att ttg gct gat gat ttc ttg agc ttg ttt gat ggc 864
 Pro Val Asn Val Ile Leu Ala Asp Asp Phe Leu Ser Leu Phe Asp Gly
 275 280 285
 ttt tct att gga tca aac gat tta acc cag ctc act tta ggc gtg gat 912
 Phe Ser Ile Gly Ser Asn Asp Leu Thr Gln Leu Thr Leu Gly Val Asp
 290 295 300
 aga gac agc gaa ttg gtc agc cat gtc ttt gat gaa agg aat gaa gcg 960
 Arg Asp Ser Glu Leu Val Ser His Val Phe Asp Glu Arg Asn Glu Ala
 305 310 315 320
 atg cta aag at 971
 Met Leu Lys
 <210> 170
 <211> 323
 <212> PRT
 <213> Helicobacter pylori
 <400> 170
 Val Ile Thr Asn Arg Gly Gly Arg Thr Cys His Ala Ala Ile Val Ala
 1 5 10 15
 Arg Glu Ile Gly Val Pro Ala Ile Val Gly Val Ser Gly Ala Thr Asp
 20 25 30
 Ser Leu Tyr Thr Gly Met Glu Ile Thr Val Ser Cys Ala Glu Gly Glu
 35 40 45
 Glu Gly Tyr Val Tyr Ala Gly Ile Tyr Glu His Glu Ile Glu Arg Val
 50 55 60
 Glu Leu Ser Asn Met Gln Glu Thr Gln Thr Lys Ile Tyr Ile Asn Ile
 65 70 75 80
 Gly Asn Pro Glu Lys Ala Phe Gly Phe Ser Gln Leu Pro Asn His Gly
 85 90 95
 Val Gly Leu Ala Arg Met Glu Met Ile Ile Leu Asn Gln Ile Lys Ala
 100 105 110
 His Pro Leu Ala Leu Val Asp Leu His His Lys Lys Ser Val Lys Glu
 115 120 125

Lys Asn Glu Ile Glu Asn Leu Met Ala Gly Tyr Ala Asn Pro Lys Asp
 130 135 140
 Phe Phe Val Lys Lys Ile Ala Glu Gly Ile Gly Met Ile Ser Ala Ala
 145 150 155 160
 Phe Tyr Pro Lys Pro Val Ile Val Arg Thr Ser Asp Phe Lys Ser Asn
 165 170 175
 Glu Tyr Met Arg Met Leu Gly Gly Ser Ser Tyr Glu Pro Asn Glu Glu
 180 185 190
 Asn Pro Met Leu Gly Tyr Arg Gly Ala Ser Arg Tyr Tyr Ser Glu Ser
 195 200 205
 Tyr Asn Glu Ala Phe Ser Trp Glu Cys Glu Ala Leu Ala Leu Val Arg
 210 215 220
 Glu Glu Met Gly Leu Thr Asn Met Lys Val Met Ile Pro Phe Leu Arg
 225 230 235 240
 Thr Ile Glu Glu Gly Lys Lys Val Leu Glu Ile Leu Arg Lys Asn Asn
 245 250 255
 Leu Glu Ser Gly Lys Asn Gly Leu Glu Ile Tyr Ile Met Cys Glu Leu
 260 265 270
 Pro Val Asn Val Ile Leu Ala Asp Asp Phe Leu Ser Leu Phe Asp Gly
 275 280 285
 Phe Ser Ile Gly Ser Asn Asp Leu Thr Gln Leu Thr Leu Gly Val Asp
 290 295 300
 Arg Asp Ser Glu Leu Val Ser His Val Phe Asp Glu Arg Asn Glu Ala
 305 310 315 320

Met Leu Lys

<210> 171

<211> 459

<212> DNA

<213> Helicobacter pylori

<220>

<221> CDS

<222> (1)..(459)

<400> 171

att tta gcg gac gac aga gcc acg act tta gag gtg atg gcc tat cac 48
 Ile Leu Ala Asp Asp Arg Ala Thr Thr Leu Glu Val Met Ala Tyr His 15
 1 5 10
 atg gaa gaa tta gaa tta aaa gat gaa gat att gcg tgt tgt ttg tat 96
 Met Glu Glu Leu Glu Leu Lys Asp Glu Asp Ile Ala Cys Cys Leu Tyr 20 25 30
 ggc gct tca gcg ctt tta caa gaa aag cat tta aaa aac gct ttt gaa 144
 Gly Ala Ser Ala Leu Leu Gln Glu Lys His Leu Lys Asn Ala Phe Glu 35 40 45
 act tta aac aaa aac caa aat acg gat tat gtt ttc aca tgc tct cca 192
 Thr Leu Asn Lys Asn Gln Asn Thr Asp Tyr Val Phe Thr Cys Ser Pro 50 55 60
 ttt agc gct tcg ccc tat cgt tct ttt agt ctt gaa aac ggc gtt caa 240
 Phe Ser Ala Ser Pro Tyr Arg Ser Phe Ser Leu Glu Asn Gly Val Gln 65 70 75 80
 atg gct ttt aaa gag cat tca aac acg cgc acg caa gat tta aaa acg 288
 Met Ala Phe Lys Glu His Ser Asn Thr Arg Thr Gln Asp Leu Lys Thr 85 90 95
 ctc tat cat gac gcg ggg ttg ctt tat atg ggg aag gct caa gcc ttt 336
 Leu Tyr His Asp Ala Gly Leu Leu Tyr Met Gly Lys Ala Gln Ala Phe 100 105 110
 aaa gaa atg cgg cct att ttt agt caa aat tct atc gct tta gaa tta 384
 Lys Glu Met Arg Pro Ile Phe Ser Gln Asn Ser Ile Ala Leu Glu Leu 115 120 125
 tcg ccc tta gaa gtc caa gat att gca cac ttt aga aga ttt aga att 432
 Ser Pro Leu Glu Val Gln Asp Ile Ala His Phe Arg Arg Phe Arg Ile 130 135 140
 agc caa gct caa ata cag ccg ttt gaa 459

Ser Gln Ala Gln Ile Gln Pro Phe Glu
145 150

<210> 172

<211> 153

<212> PRT

<213> Helicobacter pylori

<400> 172

Ile Leu Ala Asp Asp Arg Ala Thr Thr Leu Glu Val Met Ala Tyr His
1 5 10 15
Met Glu Glu Leu Glu Leu Lys Asp Glu Asp Ile Ala Cys Cys Leu Tyr
20 25 30
Gly Ala Ser Ala Leu Leu Gln Glu Lys His Leu Lys Asn Ala Phe Glu
35 40 45
Thr Leu Asn Lys Asn Gln Asn Thr Asp Tyr Val Phe Thr Cys Ser Pro
50 55 60
Phe Ser Ala Ser Pro Tyr Arg Ser Phe Ser Leu Glu Asn Gly Val Gln
65 70 75 80
Met Ala Phe Lys Glu His Ser Asn Thr Arg Thr Gln Asp Leu Lys Thr
85 90 95
Leu Tyr His Asp Ala Gly Leu Leu Tyr Met Gly Lys Ala Gln Ala Phe
100 105 110
Lys Glu Met Arg Pro Ile Phe Ser Gln Asn Ser Ile Ala Leu Glu Leu
115 120 125
Ser Pro Leu Glu Val Gln Asp Ile Ala His Phe Arg Arg Phe Arg Ile
130 135 140
Ser Gln Ala Gln Ile Gln Pro Phe Glu
145 150

<210> 173

<211> 432

<212> DNA

<213> Helicobacter pylori

<220>

<221> CDS

<222> (1)..(432)

<400> 173

gag cag aaa ttc act gaa tct aag agt tac atg gaa tgg att aaa ggc 48
Glu Gln Lys Phe Thr Glu Ser Lys Ser Tyr Met Glu Trp Ile Lys Gly
1 5 10 15
ctt tat gaa aaa agc gat ggc cct act ttg aaa tcg ttt gat cag ttt 96
Leu Tyr Glu Lys Ser Asp Gly Pro Thr Leu Lys Ser Phe Asp Gln Phe
20 25 30
tgg agg gat ggt ttt gtg gag ttt gaa atc cct gaa aat gcg aga aag 144
Trp Arg Asp Gly Phe Val Glu Phe Glu Ile Pro Glu Asn Ala Arg Lys
35 40 45
ttt gtg cgt cat gcg aaa ttc agg caa gac cct att aac aat aag ctg 192
Phe Val Arg His Ala Lys Phe Arg Gln Asp Pro Ile Asn Asn Lys Leu
50 55 60
gat aca gag agt ggg aaa att caa att ttt tct caa aaa tgc gcg gat 240
Asp Thr Glu Ser Gly Lys Ile Gln Ile Phe Ser Gln Lys Cys Ala Asp
65 70 75 80
ttt aaa ctg gcc gat ttt aaa ggg cat cct act tgg ttt gag cca gct 288
Phe Lys Leu Ala Asp Phe Lys Gly His Pro Thr Trp Phe Glu Pro Ala
85 90 95
gag tgg cta ggc tct aaa atg gct gag att tat ccg ttc cat tta atc 336
Glu Trp Leu Gly Ser Lys Met Ala Glu Ile Tyr Pro Phe His Leu Ile
100 105 110
tct ccg cac cca aaa tac cgt gtc aat tca cag ctt gat aac act tgg 384
Ser Pro His Pro Lys Tyr Arg Val Asn Ser Gln Leu Asp Asn Thr Trp
115 120 125
gtt agg aat gtg tat aaa att caa ggc aga gag cct gta atg atc aat 432
Val Arg Asn Val Tyr Lys Ile Gln Gly Arg Glu Pro Val Met Ile Asn

130 135 140

<210> 174
 <211> 144
 <212> PRT
 <213> *Helicobacter pylori*
 <400> 174

Glu Gln Lys Phe Thr Glu Ser Lys Ser Tyr Met Glu Trp Ile Lys Gly
 1 5 10 15
 Leu Tyr Glu Lys Ser Asp Gly Pro Thr Leu Lys Ser Phe Asp Gln Phe
 20 25 30
 Trp Arg Asp Gly Phe Val Glu Phe Glu Ile Pro Glu Asn Ala Arg Lys
 35 40 45
 Phe Val Arg His Ala Lys Phe Arg Gln Asp Pro Ile Asn Asn Lys Leu
 50 55 60
 Asp Thr Glu Ser Gly Lys Ile Gln Ile Phe Ser Gln Lys Cys Ala Asp
 65 70 75 80
 Phe Lys Leu Ala Asp Phe Lys Gly His Pro Thr Trp Phe Glu Pro Ala
 85 90 95
 Glu Trp Leu Gly Ser Lys Met Ala Glu Ile Tyr Pro Phe His Leu Ile
 100 105 110
 Ser Pro His Pro Lys Tyr Arg Val Asn Ser Gln Leu Asp Asn Thr Trp
 115 120 125
 Val Arg Asn Val Tyr Lys Ile Gln Gly Arg Glu Pro Val Met Ile Asn
 130 135 140

<210> 175
 <211> 1117
 <212> DNA
 <213> *Helicobacter pylori*
 <220>
 <221> CDS
 <222> (1)..(1116)
 <400> 175

cgc acg ctt gaa ttg agc ggc tat gaa gtg atg cta gta agg aat ttc 48
 Arg Thr Leu Glu Leu Ser Gly Tyr Glu Val Met Leu Val Arg Asn Phe 15
 1 5 10 15
 aca gat att gac gat aag atc atc aac aaa gcc cta aaa gaa aac aaa 96
 Thr Asp Ile Asp Asp Lys Ile Ile Asn Lys Ala Leu Lys Glu Asn Lys 30
 20 25 30
 agc att caa gaa tta agc agc att tat att gaa tct tac acg agg gat 144
 Ser Ile Gln Glu Leu Ser Ser Ile Tyr Ile Glu Ser Tyr Thr Arg Asp 45
 35 40 45
 ttg aac gct ttg aac gtg aaa aaa ccc agc cta gag cct aaa gcg agc 192
 Leu Asn Ala Leu Asn Val Lys Lys Pro Ser Leu Glu Pro Lys Ala Ser 60
 50 55 60
 gag tat tta gac gct atg gtg ggc atg att gaa acg ctt tta gaa aaa 240
 Glu Tyr Leu Asp Ala Met Val Gly Met Ile Glu Thr Leu Leu Glu Lys 75 80
 65 70 75 80
 aat atc gct tat cag gtc tct aat ggg gat att tat tta gac acg agc 288
 Asn Ile Ala Tyr Gln Val Ser Asn Gly Asp Ile Tyr Leu Asp Thr Ser 95
 85 90 95
 aag gat aaa gat tac ggc tct ttg agc gtg cat aat agc agc att gaa 336
 Lys Asp Lys Asp Tyr Gly Ser Leu Ser Val His Asn Ser Ser Ile Glu 110
 100 105 110
 ttt ggc cgt att ggt ttg gtg caa gaa aaa cgg ctt gag cag gat ttt 384
 Phe Gly Arg Ile Gly Leu Val Gln Glu Lys Arg Leu Glu Gln Asp Phe 125
 115 120 125
 gtg tta tgg aaa agc tat aag ggg gat aat gat gtg ggc ttt gat agc 432
 Val Leu Trp Lys Ser Tyr Lys Gly Asp Asn Asp Val Gly Phe Asp Ser 140
 130 135 140
 cct tta ggc aaa ggg cgc cct ggc tgg cat ata gaa tgc tct agc atg 480
 Pro Leu Gly Lys Gly Arg Pro Gly Trp His Ile Glu Cys Ser Ser Met

145 150 155 160
 gtt ttt gaa act tta gcg ctc act aac acc ccc tat caa att gat atc 528
 Val Phe Glu Thr Leu Ala Leu Thr Asn Thr Pro Tyr Gln Ile Asp Ile
 165 170 175
 cat gca ggc gga gcg gat ttg tta ttc ccc cac cat gaa aat gaa gcg 576
 His Ala Gly Gly Ala Asp Leu Leu Phe Pro His His Glu Asn Glu Ala
 180 185 190
 tgc caa acc cgt tgc gcc ttt ggc gtg gag ctt gcc aaa tat tgg atg 624
 Cys Gln Thr Arg Cys Ala Phe Gly Val Glu Leu Ala Lys Tyr Trp Met
 195 200 205
 cat aac ggc ttt gtg aat atc aat aac gaa aaa atg tct aaa agt ttg 672
 His Asn Gly Phe Val Asn Ile Asn Asn Glu Lys Met Ser Lys Ser Leu
 210 215 220
 ggg aat agc ttt ttt gtt aaa gac gct ctc aaa aac tat gat ggc gaa 720
 Gly Asn Ser Phe Phe Val Lys Asp Ala Leu Lys Asn Tyr Asp Gly Glu
 225 230 235 240
 att ttg cgc aat tac tta cta ggg gtg cat tat cgc tct gtt ttg aat 768
 Ile Leu Arg Asn Tyr Leu Leu Gly Val His Tyr Arg Ser Val Leu Asn
 245 250 255
 ttc aat gaa gaa gac ttg tta gtg agt aaa aaa cgc ttg gat aaa atc 816
 Phe Asn Glu Glu Asp Leu Leu Val Ser Lys Lys Arg Leu Asp Lys Ile
 260 265 270
 tat cgt tta aaa cag cgc gtt tta ggg act ctt gga gga ata aat cca 864
 Tyr Arg Leu Lys Gln Arg Val Leu Gly Thr Leu Gly Gly Ile Asn Pro
 275 280 285
 aac ttt aaa aaa gaa att tta gag tgc atg caa gat gat tta aac gtt 912
 Asn Phe Lys Lys Glu Ile Leu Glu Cys Met Gln Asp Asp Leu Asn Val
 290 295 300
 tct aaa gcg ttg agc gtt tta gaa agc atg ctt tct tcc act aat gaa 960
 Ser Lys Ala Leu Ser Val Leu Glu Ser Met Leu Ser Ser Thr Asn Glu
 305 310 315 320
 aaa ttg gat caa aac cct aaa aac aag gct tta aag ggc gaa att tta 1008
 Lys Leu Asp Gln Asn Pro Lys Asn Lys Ala Leu Lys Gly Glu Ile Leu
 325 330 335
 gcg aat ttg aaa ttc ata gaa gaa ctg ctt ggc atc ggg ttt aaa gac 1056
 Ala Asn Leu Lys Phe Ile Glu Glu Leu Leu Gly Ile Gly Phe Lys Asp
 340 345 350
 cct agc gcc tat ttc caa tta ggc gtg agt gaa agc gaa aaa caa gaa 1104
 Pro Ser Ala Tyr Phe Gln Leu Gly Val Ser Glu Ser Glu Lys Gln Glu
 355 360 365
 att gaa aac aag a
 Ile Glu Asn Lys
 370
 <210> 176
 <211> 372
 <212> PRT
 <213> Helicobacter pylori
 <400> 176
 Arg Thr Leu Glu Leu Ser Gly Tyr Glu Val Met Leu Val Arg Asn Phe
 1 5 10 15
 Thr Asp Ile Asp Asp Lys Ile Ile Asn Lys Ala Leu Lys Glu Asn Lys
 20 25 30
 Ser Ile Gln Glu Leu Ser Ser Ile Tyr Ile Glu Ser Tyr Thr Arg Asp
 35 40 45
 Leu Asn Ala Leu Asn Val Lys Lys Pro Ser Leu Glu Pro Lys Ala Ser
 50 55 60
 Glu Tyr Leu Asp Ala Met Val Gly Met Ile Glu Thr Leu Leu Glu Lys
 65 70 75 80
 Asn Ile Ala Tyr Gln Val Ser Asn Gly Asp Ile Tyr Leu Asp Thr Ser
 85 90 95
 Lys Asp Lys Asp Tyr Gly Ser Leu Ser Val His Asn Ser Ser Ile Glu

100 105 110
 Phe Gly Arg Ile Gly Leu Val Gln Glu Lys Arg Leu Glu Gln Asp Phe
 115 120 125
 Val Leu Trp Lys Ser Tyr Lys Gly Asp Asn Asp Val Gly Phe Asp Ser
 130 135 140
 Pro Leu Gly Lys Gly Arg Pro Gly Trp His Ile Glu Cys Ser Ser Met
 145 150 155 160
 Val Phe Glu Thr Leu Ala Leu Thr Asn Thr Pro Tyr Gln Ile Asp Ile
 165 170 175
 His Ala Gly Gly Ala Asp Leu Leu Phe Pro His His Glu Asn Glu Ala
 180 185 190
 Cys Gln Thr Arg Cys Ala Phe Gly Val Glu Leu Ala Lys Tyr Trp Met
 195 200 205
 His Asn Gly Phe Val Asn Ile Asn Asn Glu Lys Met Ser Lys Ser Leu
 210 215 220
 Gly Asn Ser Phe Phe Val Lys Asp Ala Leu Lys Asn Tyr Asp Gly Glu
 225 230 235 240
 Ile Leu Arg Asn Tyr Leu Leu Gly Val His Tyr Arg Ser Val Leu Asn
 245 250 255
 Phe Asn Glu Glu Asp Leu Leu Val Ser Lys Lys Arg Leu Asp Lys Ile
 260 265 270
 Tyr Arg Leu Lys Gln Arg Val Leu Gly Thr Leu Gly Gly Ile Asn Pro
 275 280 285
 Asn Phe Lys Lys Glu Ile Leu Glu Cys Met Gln Asp Asp Leu Asn Val
 290 295 300
 Ser Lys Ala Leu Ser Val Leu Glu Ser Met Leu Ser Ser Thr Asn Glu
 305 310 315 320
 Lys Leu Asp Gln Asn Pro Lys Asn Lys Ala Leu Lys Gly Glu Ile Leu
 325 330 335
 Ala Asn Leu Lys Phe Ile Glu Glu Leu Leu Gly Ile Gly Phe Lys Asp
 340 345 350
 Pro Ser Ala Tyr Phe Gln Leu Gly Val Ser Glu Ser Glu Lys Gln Glu
 355 360 365
 Ile Glu Asn Lys
 370
 <210> 177
 <211> 673
 <212> DNA
 <213> *Helicobacter pylori*
 <220>
 <221> CDS
 <222> (1)..(672)
 <400> 177
 gag gct aat aag caa gac gct tta ttg caa gct tta aaa gat gaa gcc 48
 Glu Ala Asn Lys Gln Asp Ala Leu Leu Gln Ala Leu Lys Asp Glu Ala
 1 5 10 15
 aac cat aaa aaa gaa aga gaa aaa aga gaa gtt aaa caa gaa gaa gaa 96
 Asn His Lys Lys Glu Arg Glu Lys Arg Glu Val Lys Gln Glu Glu Glu
 20 25 30
 att aaa gac atc aat ctg caa tta agc aaa atc aga gac agc ctg aaa 144
 Ile Lys Asp Ile Asn Leu Gln Leu Ser Lys Ile Arg Asp Ser Leu Lys
 35 40 45
 ctc att caa aac atg ttt tgg gat gag aaa aac ccc aat tct att aat 192
 Leu Ile Gln Asn Met Phe Trp Asp Glu Lys Asn Pro Asn Ser Ile Asn
 50 55 60
 atc cct caa gaa ttt gca gaa att tac aaa ctg gcc aaa caa agt ggg 240
 Ile Pro Gln Glu Phe Ala Glu Ile Tyr Lys Leu Ala Lys Gln Ser Gly
 65 70 75 80
 atg aaa ccc agc cat tta gat gaa atc atg caa ttg agc ctg gaa ttg 288
 Met Lys Pro Ser His Leu Asp Glu Ile Met Gln Leu Ser Leu Glu Leu
 85 90 95

atg cct tta cgc atg cgc gaa aat tcc gta acg att aag cgt tat ttt 336
 Met Pro Leu Arg Met Arg Glu Asn Ser Val Thr Ile Lys Arg Tyr Phe
 100 105 110
 aga gaa gtg ttg cgc aaa atg atc ttg tgt tgc cct gaa gat ttg aat 384
 Arg Glu Val Leu Arg Lys Met Ile Leu Cys Cys Pro Glu Asp Leu Asn
 115 120 125
 tta agg caa aaa cgc atc tta atg ctt gta ggg cca aca ggc gtg ggg 432
 Leu Arg Gln Lys Arg Ile Leu Met Leu Val Gly Pro Thr Gly Val Gly
 130 135 140
 aaa acg acg act tta gct aaa tta gcc gcg cgc tat tct agg atg tta 480
 Lys Thr Thr Thr Leu Ala Lys Leu Ala Arg Tyr Ser Arg Met Leu
 145 150 155 160
 gct aaa aaa tac aag gtg ggc att atc act tta gac aat tat cgc att 528
 Ala Lys Lys Tyr Lys Val Gly Ile Ile Thr Leu Asp Asn Tyr Arg Ile
 165 170 175
 ggg gct ttg gag caa tta agc tgg tat gct aat aaa atg aaa atg agt 576
 Gly Ala Leu Glu Gln Leu Ser Trp Tyr Ala Asn Lys Met Lys Met Ser
 180 185 190
 ata gaa gcg gtg att gac gct aag gat ttt gct aaa gaa att gaa gcg 624
 Ile Glu Ala Val Ile Asp Ala Lys Asp Phe Ala Lys Glu Ile Glu Ala
 195 200 205
 ttg gaa tac tgc gat ttt att tta gtg gat acg aca ggg cat tcg caa t 673
 Leu Glu Tyr Cys Asp Phe Ile Leu Val Asp Thr Thr Gly His Ser Gln
 210 215 220

<210> 178

<211> 224

<212> PRT

<213> Helicobacter pylori

<400> 178

Glu Ala Asn Lys Gln Asp Ala Leu Leu Gln Ala Leu Lys Asp Glu Ala
 1 5 10 15
 Asn His Lys Lys Glu Arg Glu Lys Arg Glu Val Lys Gln Glu Glu
 20 25 30
 Ile Lys Asp Ile Asn Leu Gln Leu Ser Lys Ile Arg Asp Ser Leu Lys
 35 40 45
 Leu Ile Gln Asn Met Phe Trp Asp Glu Lys Asn Pro Asn Ser Ile Asn
 50 55 60
 Ile Pro Gln Glu Phe Ala Glu Ile Tyr Lys Leu Ala Lys Gln Ser Gly
 65 70 75 80
 Met Lys Pro Ser His Leu Asp Glu Ile Met Gln Leu Ser Leu Glu Leu
 85 90 95
 Met Pro Leu Arg Met Arg Glu Asn Ser Val Thr Ile Lys Arg Tyr Phe
 100 105 110
 Arg Glu Val Leu Arg Lys Met Ile Leu Cys Cys Pro Glu Asp Leu Asn
 115 120 125
 Leu Arg Gln Lys Arg Ile Leu Met Leu Val Gly Pro Thr Gly Val Gly
 130 135 140
 Lys Thr Thr Thr Leu Ala Lys Leu Ala Ala Arg Tyr Ser Arg Met Leu
 145 150 155 160
 Ala Lys Lys Tyr Lys Val Gly Ile Ile Thr Leu Asp Asn Tyr Arg Ile
 165 170 175
 Gly Ala Leu Glu Gln Leu Ser Trp Tyr Ala Asn Lys Met Lys Met Ser
 180 185 190
 Ile Glu Ala Val Ile Asp Ala Lys Asp Phe Ala Lys Glu Ile Glu Ala
 195 200 205
 Leu Glu Tyr Cys Asp Phe Ile Leu Val Asp Thr Thr Gly His Ser Gln
 210 215 220

<210> 179

<211> 43

<212> DNA

<213> Helicobacter pylori

<220>

<221> CDS

<222> (1)..(42)

<400> 179

gac tat aaa gat tta gac atg ctc aag cac acg cta tca gag c 43
 Asp Tyr Lys Asp Leu Asp Met Leu Lys His Thr Leu Ser Glu
 1 5 10

<210> 180

<211> 14

<212> PRT

<213> Helicobacter pylori

<400> 180

Asp Tyr Lys Asp Leu Asp Met Leu Lys His Thr Leu Ser Glu
 1 5 10

<210> 181

<211> 238

<212> DNA

<213> Helicobacter pylori

<220>

<221> CDS

<222> (1)..(237)

<400> 181

gag cgc cta gaa aaa gaa att gaa gtc att acg aac atg aaa ttc cca 48
 Glu Arg Leu Glu Lys Glu Ile Glu Val Ile Thr Asn Met Lys Phe Pro
 1 5 10 15

ggg tat atg ctg att gtg tgg gat ttt atc cgt tat gct aag gaa atg 96
 Gly Tyr Met Leu Ile Val Trp Asp Phe Ile Arg Tyr Ala Lys Glu Met
 20 25 30

ggc att cct gta ggg cct ggt agg ggg agt gcg gcc ggg agc ttg gtg 144
 Gly Ile Pro Val Gly Pro Gly Arg Gly Ser Ala Ala Gly Ser Leu Val
 35 40 45

gct ttt gct tta aaa atc acg gat att gac cct ttg aaa tac gat ttg 192
 Ala Phe Ala Leu Lys Ile Thr Asp Ile Asp Pro Leu Lys Tyr Asp Leu
 50 55 60

ctc ttt gaa agg ttt tta aac ccc gaa aga atc agc atg cct gat a 238
 Leu Phe Glu Arg Phe Leu Asn Pro Glu Arg Ile Ser Met Pro Asp
 65 70 75

<210> 182

<211> 79

<212> PRT

<213> Helicobacter pylori

<400> 182

Glu Arg Leu Glu Lys Glu Ile Glu Val Ile Thr Asn Met Lys Phe Pro
 1 5 10 15

Gly Tyr Met Leu Ile Val Trp Asp Phe Ile Arg Tyr Ala Lys Glu Met
 20 25 30

Gly Ile Pro Val Gly Pro Gly Arg Gly Ser Ala Ala Gly Ser Leu Val
 35 40 45

Ala Phe Ala Leu Lys Ile Thr Asp Ile Asp Pro Leu Lys Tyr Asp Leu
 50 55 60

Leu Phe Glu Arg Phe Leu Asn Pro Glu Arg Ile Ser Met Pro Asp
 65 70 75

<210> 183

<211> 1588

<212> DNA

<213> Helicobacter pylori

<220>

<221> CDS

<222> (1)..(1587)

<400> 183

aat tta ggg aat gca aac aac acc att tac tat tac gac aag agc att 48

Asn	Leu	Gly	Asn	Ala	Asn	Asn	Thr	Ile	Tyr	Tyr	Tyr	Asp	Lys	Ser	Ile	
1				5					10					15		
gat	ttt	tat	gcg	agc	ggg	aaa	act	cta	ttc	act	aaa	gcg	gaa	ttt	tct	96
Asp	Phe	Tyr	Ala	Ser	Gly	Lys	Thr	Leu	Phe	Thr	Lys	Ala	Glu	Phe	Ser	
			20					25					30			
caa	aca	ttc	acc	ggg	caa	aac	agc	gcg	atc	gtt	ttt	ggg	gct	aaa	agc	144
Gln	Thr	Phe	Thr	Gly	Gln	Asn	Ser	Ala	Ile	Val	Phe	Gly	Ala	Lys	Ser	
			35				40					45				
ata	tgg	acg	agc	tta	agc	gat	gca	ccg	cag	tct	aac	acc	atc	att	cgc	192
Ile	Trp	Thr	Ser	Leu	Ser	Asp	Ala	Pro	Gln	Ser	Asn	Thr	Ile	Ile	Arg	
	50					55					60					
ttt	ggg	gac	aat	aag	gga	gca	ggg	agt	aat	gat	gcg	agc	ggg	cat	tgc	240
Phe	Gly	Asp	Asn	Lys	Gly	Ala	Gly	Ser	Asn	Asp	Ala	Ser	Gly	His	Cys	
	65				70					75				80		
tgg	aat	ttg	caa	tgc	ata	ggc	ttt	att	aca	ggg	cat	tat	gaa	gcg	caa	288
Trp	Asn	Leu	Gln	Cys	Ile	Gly	Phe	Ile	Thr	Gly	His	Tyr	Glu	Ala	Gln	
				85					90					95		
aag	att	tac	atc	acc	ggt	agc	att	gaa	agc	ggg	aat	cgc	att	tct	agc	336
Lys	Ile	Tyr	Ile	Thr	Gly	Ser	Ile	Glu	Ser	Gly	Asn	Arg	Ile	Ser	Ser	
			100					105					110			
ggt	ggg	ggc	gcg	agc	ctt	aat	ttt	aac	ggg	ctt	caa	ggc	att	ctt	tta	384
Gly	Gly	Gly	Ala	Ser	Leu	Asn	Phe	Asn	Gly	Leu	Gln	Gly	Ile	Leu	Leu	
			115				120					125				
acg	aac	gcg	act	ttg	tat	aac	cgc	gcc	gct	ggc	acg	caa	agc	tcg	tct	432
Thr	Asn	Ala	Thr	Leu	Tyr	Asn	Arg	Ala	Ala	Gly	Thr	Gln	Ser	Ser	Ser	
			130				135				140					
atg	aat	ttt	atc	tct	aac	agc	gcg	aac	att	cag	gct	caa	aac	tcc	tat	480
Met	Asn	Phe	Ile	Ser	Asn	Ser	Ala	Asn	Ile	Gln	Ala	Gln	Asn	Ser	Tyr	
	145				150					155				160		
ttt	ata	gac	gat	acc	gca	caa	aat	ggc	ggt	aac	cct	aat	ttc	agt	ttc	528
Phe	Ile	Asp	Asp	Thr	Ala	Gln	Asn	Gly	Gly	Asn	Pro	Asn	Phe	Ser	Phe	
				165				170						175		
aac	gct	ttg	aat	ctg	gat	ttt	tct	aac	agc	tct	ttt	aga	ggc	tat	gtg	576
Asn	Ala	Leu	Asn	Leu	Asp	Phe	Ser	Asn	Ser	Ser	Phe	Arg	Gly	Tyr	Val	
			180					185					190			
ggg	aaa	acg	caa	tct	ggt	ttt	aaa	ttc	aat	gcc	aag	aat	gcg	atc	agt	624
Gly	Lys	Thr	Gln	Ser	Val	Phe	Lys	Phe	Asn	Ala	Lys	Asn	Ala	Ile	Ser	
			195				200					205				
ttc	acc	aac	agc	acg	aat	tta	agc	tct	ggt	ttg	tat	caa	atg	caa	gct	672
Phe	Thr	Asn	Ser	Thr	Asn	Leu	Ser	Ser	Gly	Leu	Tyr	Gln	Met	Gln	Ala	
			210			215					220					
aaa	agc	gtg	ttg	ttt	gac	aat	tcc	aat	tta	agc	ggt	tca	gtg	ggg	aca	720
Lys	Ser	Val	Leu	Phe	Asp	Asn	Ser	Asn	Leu	Ser	Val	Ser	Val	Gly	Thr	
	225				230					235				240		
agc	agt	att	aaa	gcc	aat	gcg	atc	aat	ctt	tct	caa	aat	gcc	tct	att	768
Ser	Ser	Ile	Lys	Ala	Asn	Ala	Ile	Asn	Leu	Ser	Gln	Asn	Ala	Ser	Ile	
				245				250						255		
aat	gcg	agc	aac	cat	tca	acc	tta	gaa	ctt	caa	ggc	gat	ttg	aat	gtg	816
Asn	Ala	Ser	Asn	His	Ser	Thr	Leu	Glu	Leu	Gln	Gly	Asp	Leu	Asn	Val	
			260					265					270			
aac	gac	acc	agc	tcg	ctc	aac	ctc	aac	caa	agc	acg	att	aat	ggt	tcc	864
Asn	Asp	Thr	Ser	Ser	Leu	Asn	Leu	Asn	Gln	Ser	Thr	Ile	Asn	Val	Ser	
			275				280					285				
aat	aac	gcc	acg	atc	aac	gat	tat	gcg	agc	ttg	att	gcg	agt	aat	ggc	912
Asn	Asn	Ala	Thr	Ile	Asn	Asp	Tyr	Ala	Ser	Leu	Ile	Ala	Ser	Asn	Gly	
			290			295					300					
tct	cac	ctt	aat	ttt	aac	ggg	gcg	ggt	aat	ttc	aat	tca	gcg	aat	att	960
Ser	His	Leu	Asn	Phe	Asn	Gly	Ala	Val	Asn	Phe	Asn	Ser	Ala	Asn	Ile	
				310						315				320		
act	acg	agt	ttg	aat	aat	tcc	tct	atc	gtg	ttt	aag	ggg	gcg	gtc	tct	1008
Thr	Thr	Ser	Leu	Asn	Asn	Ser	Ser	Ile	Val	Phe	Lys	Gly	Ala	Val	Ser	

325 330 335
 tta gga ggg cag ttt aat tta agc aat aac tct tct tta gat ttc caa 1056
 Leu Gly Gly Gln Phe Asn Leu Ser Asn Asn Ser Ser Leu Asp Phe Gln
 340 345 350
 ggc tct agc gct atc acc tct aac acg gcg ttt aat ttc tat gat aac 1104
 Gly Ser Ser Ala Ile Thr Ser Asn Thr Ala Phe Asn Phe Tyr Asp Asn
 355 360 365
 gct ttt tct caa agc ccc atc act ttc cat caa gcc ctt gac att aaa 1152
 Ala Phe Ser Gln Ser Pro Ile Thr Phe His Gln Ala Leu Asp Ile Lys
 370 375 380
 gcg ccc tta agt ttg gga ggc aac ctt tta aac cct aac aac agc agc 1200
 Ala Pro Leu Ser Leu Gly Gly Asn Leu Leu Asn Pro Asn Asn Ser Ser
 385 390 395 400
 gtg ctg gat tta aaa aac agc cag ctt gtt ttt ggc gat caa ggg agt 1248
 Val Leu Asp Leu Lys Asn Ser Gln Leu Val Phe Gly Asp Gln Gly Ser
 405 410 415
 ttg aat atc gct aac att gat tta cta agc gat cta aat gat aat aaa 1296
 Leu Asn Ile Ala Asn Ile Asp Leu Leu Ser Asp Leu Asn Asp Asn Lys
 420 425 430
 aat cgt gtg tat aac atc att caa gcg gac atg aat agt aat tgg tat 1344
 Asn Arg Val Tyr Asn Ile Ile Gln Ala Asp Met Asn Ser Asn Trp Tyr
 435 440 445
 gag cgt atc agc ttc ttt ggc atg cac atc aat gac ggg att tat gat 1392
 Glu Arg Ile Ser Phe Phe Gly Met His Ile Asn Asp Gly Ile Tyr Asp
 450 455 460
 gct aaa aac caa act tat agt ttc act aac ccc ctt aat aac gcc cta 1440
 Ala Lys Asn Gln Thr Tyr Ser Phe Thr Asn Pro Leu Asn Asn Ala Leu
 465 470 475 480
 aaa atc acc gag agc ttt aaa gac aac caa cta agc gtt acg ctc tct 1488
 Lys Ile Thr Glu Ser Phe Lys Asp Asn Gln Leu Ser Val Thr Leu Ser
 485 490 495
 caa atc ccg ggt att aaa aac acg ctc tat aac att ggc tct gaa att 1536
 Gln Ile Pro Gly Ile Lys Asn Thr Leu Tyr Asn Ile Gly Ser Glu Ile
 500 505 510
 ttt aac tac caa aaa gtt tat aac aac gct aat ggc gtg tat tct tat 1584
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 515 520 525
 agc g 1588
 Ser
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 35 40 45
 Ile Trp Thr Ser Leu Ser Asp Ala Pro Gln Ser Asn Thr Ile Ile Arg
 50 55 60
 Phe Gly Asp Asn Lys Gly Ala Gly Ser Asn Asp Ala Ser Gly His Cys
 65 70 75 80
 Trp Asn Leu Gln Cys Ile Gly Phe Ile Thr Gly His Tyr Glu Ala Gln
 85 90 95
 Lys Ile Tyr Ile Thr Gly Ser Ile Glu Ser Gly Asn Arg Ile Ser Ser
 100 105 110
 Gly Gly Gly Ala Ser Leu Asn Phe Asn Gly Leu Gln Gly Ile Leu Leu
 115 120 125
 Thr Asn Ala Thr Leu Tyr Asn Arg Ala Ala Gly Thr Gln Ser Ser Ser

130 135 140
 Met Asn Phe Ile Ser Asn Ser Ala Asn Ile Gln Ala Gln Asn Ser Tyr
 145 150 155 160
 Phe Ile Asp Asp Thr Ala Gln Asn Gly Gly Asn Pro Asn Phe Ser Phe
 165 170 175
 Asn Ala Leu Asn Leu Asp Phe Ser Asn Ser Ser Phe Arg Gly Tyr Val
 180 185 190
 Gly Lys Thr Gln Ser Val Phe Lys Phe Asn Ala Lys Asn Ala Ile Ser
 195 200 205
 Phe Thr Asn Ser Thr Asn Leu Ser Ser Gly Leu Tyr Gln Met Gln Ala
 210 215 220
 Lys Ser Val Leu Phe Asp Asn Ser Asn Leu Ser Val Ser Val Gly Thr
 225 230 235 240
 Ser Ser Ile Lys Ala Asn Ala Ile Asn Leu Ser Gln Asn Ala Ser Ile
 245 250 255
 Asn Ala Ser Asn His Ser Thr Leu Glu Leu Gln Gly Asp Leu Asn Val
 260 265 270
 Asn Asp Thr Ser Ser Leu Asn Leu Asn Gln Ser Thr Ile Asn Val Ser
 275 280 285
 Asn Asn Ala Thr Ile Asn Asp Tyr Ala Ser Leu Ile Ala Ser Asn Gly
 290 295 300
 Ser His Leu Asn Phe Asn Gly Ala Val Asn Phe Asn Ser Ala Asn Ile
 305 310 315 320
 Thr Thr Ser Leu Asn Asn Ser Ser Ile Val Phe Lys Gly Ala Val Ser
 325 330 335
 Leu Gly Gly Gln Phe Asn Leu Ser Asn Asn Ser Ser Leu Asp Phe Gln
 340 345 350
 Gly Ser Ser Ala Ile Thr Ser Asn Thr Ala Phe Asn Phe Tyr Asp Asn
 355 360 365
 Ala Phe Ser Gln Ser Pro Ile Thr Phe His Gln Ala Leu Asp Ile Lys
 370 375 380
 Ala Pro Leu Ser Leu Gly Gly Asn Leu Leu Asn Pro Asn Asn Ser Ser
 385 390 395 400
 Val Leu Asp Leu Lys Asn Ser Gln Leu Val Phe Gly Asp Gln Gly Ser
 405 410 415
 Leu Asn Ile Ala Asn Ile Asp Leu Leu Ser Asp Leu Asn Asp Asn Lys
 420 425 430
 Asn Arg Val Tyr Asn Ile Ile Gln Ala Asp Met Asn Ser Asn Trp Tyr
 435 440 445
 Glu Arg Ile Ser Phe Phe Gly Met His Ile Asn Asp Gly Ile Tyr Asp
 450 455 460
 Ala Lys Asn Gln Thr Tyr Ser Phe Thr Asn Pro Leu Asn Asn Ala Leu
 465 470 475 480
 Lys Ile Thr Glu Ser Phe Lys Asp Asn Gln Leu Ser Val Thr Leu Ser
 485 490 495
 Gln Ile Pro Gly Ile Lys Asn Thr Leu Tyr Asn Ile Gly Ser Glu Ile
 500 505 510
 Phe Asn Tyr Gln Lys Val Tyr Asn Asn Ala Asn Gly Val Tyr Ser Tyr
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Ser

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<211> 1735

<212> DNA

<213> Helicobacter pylori

<220>

<221> CDS

<222> (1)..(1734)

<400> 185

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gat aat ttt tta gaa atc aat aat cgt gtg ggt tct gga gcc ggg agg				96
Asp Asn Phe Leu Glu Ile Asn Asn Arg Val Gly Ser Gly Ala Gly Arg				
20	25	30		
aaa gcc agc tct acg gtt tta act ttg caa gct tca gaa ggg att act				144
Lys Ala Ser Ser Thr Val Leu Thr Leu Gln Ala Ser Glu Gly Ile Thr				
35	40	45		
agc agt aaa aat gcg gaa att tct ctt tat gat ggc gcc acg ctc aat				192
Ser Ser Lys Asn Ala Glu Ile Ser Leu Tyr Asp Gly Ala Thr Leu Asn				
50	55	60		
ttg gct tca aac agc gtt aaa tta atg ggt aat gtg tgg atg ggc cgt				240
Leu Ala Ser Asn Ser Val Lys Leu Met Gly Asn Val Trp Met Gly Arg				
65	70	75	80	
ttg caa tat gtg gga gcg tat ttg gcc cct tca tac agc acg ata aac				288
Leu Gln Tyr Val Gly Ala Tyr Leu Ala Pro Ser Tyr Ser Thr Ile Asn				
85	90	95		
act tca aaa gtg aca ggg gaa gtg aat ttt aac cat ctc act gtg ggc				336
Thr Ser Lys Val Thr Gly Glu Val Asn Phe Asn His Leu Thr Val Gly				
100	105	110		
gat cac aac gcc gct caa gca ggc att atc gct agt aac aag act cat				384
Asp His Asn Ala Ala Gln Ala Gly Ile Ile Ala Ser Asn Lys Thr His				
115	120	125		
att ggc aca ctg gat ttg tgg caa agc gcg gga cta aac att atc gcc				432
Ile Gly Thr Leu Asp Leu Trp Gln Ser Ala Gly Leu Asn Ile Ile Ala				
130	135	140		
cct cca gaa ggc ggt tat aag gat aaa cct aag gat aaa cct agt aac				480
Pro Pro Glu Gly Gly Tyr Lys Asp Lys Pro Lys Asp Lys Pro Ser Asn				
145	150	155	160	
acc acg caa aat aat gct aac aac aac caa caa aac agc gct caa aac				528
Thr Thr Gln Asn Asn Ala Asn Asn Asn Gln Gln Asn Ser Ala Gln Asn				
165	170	175		
aat agt aac act cag gtt att aac cca ccc aat agc gcg caa aaa aca				576
Asn Ser Asn Thr Gln Val Ile Asn Pro Pro Asn Ser Ala Gln Lys Thr				
180	185	190		
gaa att caa ccc acg caa gtc att gat ggg cct ttt gct ggt ggc aaa				624
Glu Ile Gln Pro Thr Gln Val Ile Asp Gly Pro Phe Ala Gly Gly Lys				
195	200	205		
gac acg gtt gtc aat att gat cgc atc aac act aac gct gat ggc acg				672
Asp Thr Val Val Asn Ile Asp Arg Ile Asn Thr Asn Ala Asp Gly Thr				
210	215	220		
att aaa gtg gga ggg tat aaa gct tct ctt acc acc aat gcg gct cat				720
Ile Lys Val Gly Gly Tyr Lys Ala Ser Leu Thr Thr Asn Ala Ala His				
225	230	235	240	
ttg cat atc ggc aaa ggc ggt atc aat ctg tcc aat caa gcg agc ggg				768
Leu His Ile Gly Lys Gly Gly Ile Asn Leu Ser Asn Gln Ala Ser Gly				
245	250	255		
cgc acc ctt tta gtg gaa aat cta acc ggg aat atc acc gtt gat ggg				816
Arg Thr Leu Leu Val Glu Asn Leu Thr Gly Asn Ile Thr Val Asp Gly				
260	265	270		
cct tta aga gtg aat aat caa gtg ggt ggt tat gct ttg gca gga tca				864
Pro Leu Arg Val Asn Asn Gln Val Gly Gly Tyr Ala Leu Ala Gly Ser				
275	280	285		
agc gcg aat ttt gag ttt aag gct ggt acg gat acc aaa aac ggc aca				912
Ser Ala Asn Phe Glu Phe Lys Ala Gly Thr Asp Thr Lys Asn Gly Thr				
290	295	300		
gcc act ttt aat aac gat att agt ttg gga aga ttt gtg aat tta aaa				960
Ala Thr Phe Asn Asn Ile Ser Leu Gly Arg Phe Val Asn Leu Lys				
305	310	315	320	
gtg gat gct cat aca gct aat ttt aaa ggt att gat act ggt aat ggt				1008
Val Asp Ala His Thr Ala Asn Phe Lys Gly Ile Asp Thr Gly Asn Gly				
325	330	335		

ggt ttc aac acc tta gat ttt agt ggc gtt aca ggt aag gtc aat atc 1056
 Gly Phe Asn Thr Leu Asp Phe Ser Gly Val Thr Gly Lys Val Asn Ile
 340 345 350
 aac aag ctc att acg gct tcc act aat gtg gcc gtt aaa aac ttc aac 1104
 Asn Lys Leu Ile Thr Ala Ser Thr Asn Val Ala Val Lys Asn Phe Asn
 355 360 365
 att aat gaa ttg gtt gtt aag acc aat ggg gtg agt gtg ggg gaa tac 1152
 Ile Asn Glu Leu Val Val Lys Thr Asn Gly Val Ser Val Gly Glu Tyr
 370 375 380
 act cat ttt agc gaa gat ata ggc agt caa tcg cgc atc aat acc gtg 1200
 Thr His Phe Ser Glu Asp Ile Gly Ser Gln Ser Arg Ile Asn Thr Val
 385 390 395 400
 cgt ttg gaa act ggc act agg tca atc ttt tct ggg ggt gtc aaa ttt 1248
 Arg Leu Glu Thr Gly Thr Arg Ser Ile Phe Ser Gly Gly Val Lys Phe
 405 410 415
 aaa agc ggt gaa aaa ctg gtt ata gat gag ttt tac tat agc cct tgg 1296
 Lys Ser Gly Glu Lys Leu Val Ile Asp Glu Phe Tyr Tyr Ser Pro Trp
 420 425 430
 aat tat ttt gac gct agg aat att aaa aat gtt gaa atc acc aga aaa 1344
 Asn Tyr Phe Asp Ala Arg Asn Ile Lys Asn Val Glu Ile Thr Arg Lys
 435 440 445
 ttc gct tct tca acc cca gaa aac cct tgg ggc aca tca aag ctt atg 1392
 Phe Ala Ser Ser Thr Pro Glu Asn Pro Trp Gly Thr Ser Lys Leu Met
 450 455 460
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 Phe Asn Asn Leu Thr Leu Gly Gln Asn Ala Val Met Asp Tyr Ser Gln
 465 470 475 480
 ttt tca aat tta acc att cag ggg gat ttc atc aac aat caa ggc act 1488
 Phe Ser Asn Leu Thr Ile Gln Gly Asp Phe Ile Asn Asn Gln Gly Thr
 485 490 495
 atc aat tat ttg gtc cga ggc ggg caa gta gcc acc ttg aat gta ggc 1536
 Ile Asn Tyr Leu Val Arg Gly Gly Gln Val Ala Thr Leu Asn Val Gly
 500 505 510
 aat gcg gca gct atg ttc ttt agt aat aat gtg gat agc gcg act ggg 1584
 Asn Ala Ala Ala Met Phe Phe Ser Asn Asn Val Asp Ser Ala Thr Gly
 515 520 525
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 Phe Tyr Gln Pro Leu Met Lys Ile Asn Ser Ala Gln Asp Leu Ile Lys
 530 535 540
 aat aaa gaa cat gtc tta ttg aaa gcg aaa atc atc ggt tat ggc aat 1680
 Asn Lys Glu His Val Leu Leu Lys Ala Lys Ile Ile Gly Tyr Gly Asn
 545 550 555 560
 gtt tct tta ggc act aac agc att agt aat gtt aat cta ata gag caa 1728
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 Phe Lys
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 Lys Ala Ser Ser Thr Val Leu Thr Leu Gln Ala Ser Glu Gly Ile Thr
 35 40 45
 Ser Ser Lys Asn Ala Glu Ile Ser Leu Tyr Asp Gly Ala Thr Leu Asn
 50 55 60
 Leu Ala Ser Asn Ser Val Lys Leu Met Gly Asn Val Trp Met Gly Arg

Val Ser Leu Gly Thr Asn Ser Ile Ser Asn Val Asn Leu Ile Glu Gln
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Phe Lys

<210> 187

<211> 666

<212> DNA

<213> Helicobacter pylori

<220>

<221> CDS

<222> (1)..(666)

<400> 187

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gaa atc aag gct aaa gtg gct tat gtg aaa atc ccc caa tta gaa gat 96
Glu Ile Lys Ala Lys Val Ala Tyr Val Lys Ile Pro Gln Leu Glu Asp
20 25 30
ttg gaa aac aac ccg gtt tat atc ggt caa att ata ggc gta act tat 144
Leu Glu Asn Asn Pro Val Tyr Ile Gly Gln Ile Ile Gly Val Thr Tyr
35 40 45
gat tta ttg ctg ttt gac gct gag ttt ttg gaa gcc aaa atc aaa gac 192
Asp Leu Leu Leu Phe Asp Ala Glu Phe Leu Glu Ala Lys Ile Lys Asp
50 55 60
ggg ttg gat aaa acc caa att gag ctt tta aac aag atg cct aaa tgg 240
Gly Leu Asp Lys Thr Gln Ile Glu Leu Leu Asn Lys Met Pro Lys Trp
65 70 75 80
aaa aag gtg gaa aaa gag ctt ttc aga gcg act tat tat tac aag att 288
Lys Lys Val Glu Lys Glu Leu Phe Arg Ala Thr Tyr Tyr Tyr Lys Ile
85 90 95
aag ggc ata aaa gcg att att ccg tcc tta gaa gtg agc gcg ttt tcc 336
Lys Gly Ile Lys Ala Ile Ile Pro Ser Leu Glu Val Ser Ala Phe Ser
100 105 110
aat aaa gac aaa tac ata gat cat tcc ata gcc cca aaa gtt act ttg 384
Asn Lys Asp Lys Tyr Ile Asp His Ser Ile Ala Pro Lys Val Thr Leu
115 120 125
cag gta acg gat ttg tcc aaa aac cct cgt tat gcg aat gtc atg gct 432
Gln Val Thr Asp Leu Ser Lys Asn Pro Arg Tyr Ala Asn Val Met Ala
130 135 140
aaa gat tta caa gtc ttg caa tac aaa acc aaa gat tat gac gat aaa 480
Lys Asp Leu Gln Val Leu Gln Tyr Lys Thr Lys Asp Tyr Asp Asp Lys
145 150 155 160
aac aat att ttg gtg atg gaa ata gcg ttc aaa gaa gcc act tgg gaa 528
Asn Asn Ile Leu Val Met Glu Ile Ala Phe Lys Glu Ala Thr Trp Glu
165 170 175
gat ttt cac atc aaa gaa gcg atc aag caa ggg ttt gat aac gcc tct 576
Asp Phe His Ile Lys Glu Ala Ile Lys Gln Gly Phe Asp Asn Ala Ser
180 185 190
tta aac cag atc aag gct aaa gaa ggg agc gtt ttt tat tat tgc gtg 624
Leu Asn Gln Ile Lys Ala Lys Glu Gly Ser Val Phe Tyr Tyr Cys Val
195 200 205
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<212> PRT

<213> Helicobacter pylori

<400> 188

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 35 40 45
 Asp Leu Leu Leu Phe Asp Ala Glu Phe Leu Glu Ala Lys Ile Lys Asp
 50 55 60
 Gly Leu Asp Lys Thr Gln Ile Glu Leu Leu Asn Lys Met Pro Lys Trp
 65 70 75 80
 Lys Lys Val Glu Lys Glu Leu Phe Arg Ala Thr Tyr Tyr Tyr Lys Ile
 85 90 95
 Lys Gly Ile Lys Ala Ile Ile Pro Ser Leu Glu Val Ser Ala Phe Ser
 100 105 110
 Asn Lys Asp Lys Tyr Ile Asp His Ser Ile Ala Pro Lys Val Thr Leu
 115 120 125
 Gln Val Thr Asp Leu Ser Lys Asn Pro Arg Tyr Ala Asn Val Met Ala
 130 135 140
 Lys Asp Leu Gln Val Leu Gln Tyr Lys Thr Lys Asp Tyr Asp Asp Lys
 145 150 155 160
 Asn Asn Ile Leu Val Met Glu Ile Ala Phe Lys Glu Ala Thr Trp Glu
 165 170 175
 Asp Phe His Ile Lys Glu Ala Ile Lys Gln Gly Phe Asp Asn Ala Ser
 180 185 190
 Leu Asn Gln Ile Lys Ala Lys Glu Gly Ser Val Phe Tyr Tyr Cys Val
 195 200 205
 Leu Pro Lys Thr Ile Gln Asn Leu Ser Phe Asp Tyr Phe Ser
 210 215 220

<210> 189

<211> 186

<212> DNA

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<222> (1)..(186)

<400> 189

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 att gag ctt tcc acc gtg aat tat tta gcc cct tta att ttc aat ttg 96
 Ile Glu Leu Ser Thr Val Asn Tyr Leu Ala Pro Leu Ile Phe Asn Leu
 20 25 30
 gac aag cag ctc atg ggg caa gtg gtt ttg gat tct aac aaa tac cca 144
 Asp Lys Gln Leu Met Gly Gln Val Val Leu Asp Ser Asn Lys Tyr Pro
 35 40 45
 cac tac cat tta aga gag aat att cta agc cac acg cat gaa 186
 His Tyr His Leu Arg Glu Asn Ile Leu Ser His Thr His Glu
 50 55 60

<210> 190

<211> 62

<212> PRT

<213> Helicobacter pylori

<400> 190

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 20 25 30
 Asp Lys Gln Leu Met Gly Gln Val Val Leu Asp Ser Asn Lys Tyr Pro
 35 40 45
 His Tyr His Leu Arg Glu Asn Ile Leu Ser His Thr His Glu
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<210> 191

<211> 864

<212> DNA

<213> *Helicobacter pylori*

<220>

<221> CDS

<222> (1)..(864)

<400> 191

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ggg ttc atc tat gag atc agc gag ttc atg aaa gcc tat acc gca ttg 96
Gly Phe Ile Tyr Glu Ile Ser Glu Phe Met Lys Ala Tyr Thr Ala Leu
          20           25           30
cta aaa aaa caa gac cga tac gtc tat tta ttg agg tat ctc ccc tct 144
Leu Lys Lys Gln Asp Arg Tyr Val Tyr Leu Leu Arg Tyr Leu Pro Ser
          35           40           45
agg tat tgg gcc agc att tta acg act gcc ctt tat gtc aaa tac cct 192
Arg Tyr Trp Ala Ser Ile Leu Thr Thr Ala Leu Tyr Val Lys Tyr Pro
          50           55           60
gat ttt gac gct ttg aaa aag ctt ttg gtg tct tat tat tac caa act 240
Asp Phe Asp Ala Leu Lys Lys Leu Leu Val Ser Tyr Tyr Tyr Gln Thr
          65           70           75           80
tgg att gca gga ggc acg atc acg cgc atc aag caa acc agt atc aac 288
Trp Ile Ala Gly Gly Thr Ile Thr Arg Ile Lys Gln Thr Ser Ile Asn
          85           90           95
att atc aaa aac gtt aaa agc aat aag agc gtt gaa acc atc aaa gag 336
Ile Ile Lys Asn Val Lys Ser Asn Lys Ser Val Glu Thr Ile Lys Glu
          100          105          110
ctt ata ttg aat agc atc gac tct tat aac acc ttt gat caa tac ctc 384
Leu Ile Leu Asn Ser Ile Asp Ser Tyr Asn Thr Phe Asp Gln Tyr Leu
          115          120          125
tat aac tta tgg gat agc tct tct gtt tat cat agc aaa tgg gtg cgt 432
Tyr Asn Leu Trp Asp Ser Ser Ser Val Tyr His Ser Lys Trp Val Arg
          130          135          140
cct gtc tta gcc cta gct aat tat ttc atg gca gat gaa gag aaa ccc 480
Pro Val Leu Ala Leu Ala Asn Tyr Phe Met Ala Asp Glu Glu Lys Pro
          145          150          155          160
cat ttt atc gct atg gat gcc gaa acc caa gtg gag cat att ttg cca 528
His Phe Ile Ala Met Asp Ala Glu Thr Gln Val Glu His Ile Leu Pro
          165          170          175
caa acg ccc aaa aga ggc agt caa tgg aac gcg gat ttt gac aaa gaa 576
Gln Thr Pro Lys Arg Gly Ser Gln Trp Asn Ala Asp Phe Asp Lys Glu
          180          185          190
aaa aga gaa gaa tgg gta aat aat atc gcg aat tta acc ctt tta aag 624
Lys Arg Glu Glu Trp Val Asn Asn Ile Ala Asn Leu Thr Leu Leu Lys
          195          200          205
cgt aaa aag aac gcg cat gct tta aac ggg gat ttt gat gaa aaa aga 672
Arg Lys Lys Asn Ala His Ala Leu Asn Gly Asp Phe Asp Glu Lys Arg
          210          215          220
aaa att tat gga ggc aaa gac acg agc aaa gtg att agc tgt tat gac 720
Lys Ile Tyr Gly Gly Lys Asp Thr Ser Lys Val Ile Ser Cys Tyr Asp
          225          230          235          240
atc act aaa gaa ttg tat agc aat tat agg aag tgg aat gag aag tcc 768
Ile Thr Lys Glu Leu Tyr Ser Asn Tyr Arg Lys Trp Asn Glu Lys Ser
          245          250          255
ctc caa gag cga tac aaa tct ttg tat aac act atc acg cct gtt tta 816
Leu Gln Glu Arg Tyr Lys Ser Leu Tyr Asn Thr Ile Thr Pro Val Leu
          260          265          270
cac ata gag ggg caa gaa gat gat ttt gaa gat gat ttt gat cta gaa 864
His Ile Glu Gly Gln Glu Asp Asp Phe Glu Asp Asp Phe Asp Leu Glu
          275          280          285

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<210> 192

<211> 288

<212> PRT

<213> *Helicobacter pylori*

<400> 192

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Gly Phe Ile Tyr Glu Ile Ser Glu Phe Met Lys Ala Tyr Thr Ala Leu
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Leu Lys Lys Gln Asp Arg Tyr Val Tyr Leu Leu Arg Tyr Leu Pro Ser
      35           40           45
Arg Tyr Trp Ala Ser Ile Leu Thr Thr Ala Leu Tyr Val Lys Tyr Pro
      50           55           60
Asp Phe Asp Ala Leu Lys Lys Leu Leu Val Ser Tyr Tyr Tyr Gln Thr
      65           70           75           80
Trp Ile Ala Gly Gly Thr Ile Thr Arg Ile Lys Gln Thr Ser Ile Asn
      85           90           95
Ile Ile Lys Asn Val Lys Ser Asn Lys Ser Val Glu Thr Ile Lys Glu
      100          105          110
Leu Ile Leu Asn Ser Ile Asp Ser Tyr Asn Thr Phe Asp Gln Tyr Leu
      115          120          125
Tyr Asn Leu Trp Asp Ser Ser Ser Val Tyr His Ser Lys Trp Val Arg
      130          135          140
Pro Val Leu Ala Leu Ala Asn Tyr Phe Met Ala Asp Glu Glu Lys Pro
      145          150          155          160
His Phe Ile Ala Met Asp Ala Glu Thr Gln Val Glu His Ile Leu Pro
      165          170          175
Gln Thr Pro Lys Arg Gly Ser Gln Trp Asn Ala Asp Phe Asp Lys Glu
      180          185          190
Lys Arg Glu Glu Trp Val Asn Asn Ile Ala Asn Leu Thr Leu Leu Lys
      195          200          205
Arg Lys Lys Asn Ala His Ala Leu Asn Gly Asp Phe Asp Glu Lys Arg
      210          215          220
Lys Ile Tyr Gly Gly Lys Asp Thr Ser Lys Val Ile Ser Cys Tyr Asp
      225          230          235          240
Ile Thr Lys Glu Leu Tyr Ser Asn Tyr Arg Lys Trp Asn Glu Lys Ser
      245          250          255
Leu Gln Glu Arg Tyr Lys Ser Leu Tyr Asn Thr Ile Thr Pro Val Leu
      260          265          270
His Ile Glu Gly Gln Glu Asp Asp Phe Glu Asp Asp Phe Asp Leu Glu
      275          280          285

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<210> 193

<211> 417

<212> DNA

<213> *Helicobacter pylori*

<220>

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<222> (1)..(417)

<400> 193

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tca cgc aaa aat agg gcg cga aat ttt atg cca aga atg cca aaa gat   96
Ser Arg Lys Asn Arg Ala Arg Asn Phe Met Pro Arg Met Pro Lys Asp
      20           25           30
tcg cac tcg caa ggc ttt gag act tta agc att aat ttt gaa ggc acg   144
Ser His Ser Gln Gly Phe Glu Thr Leu Ser Ile Asn Phe Glu Gly Thr
      35           40           45
atg gag tgg agc gcg ttt ggg att tgg ctg agt ttg tta ttg cat caa   192
Met Glu Trp Ser Ala Phe Gly Ile Trp Leu Ser Leu Leu Leu His Gln
      50           55           60
tac ggc aca cag att tta cgc atc aag ggg att att gac att gga agc   240

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Tyr Gly Thr Gln Ile Leu Arg Ile Lys Gly Ile Ile Asp Ile Gly Ser
 65 70 75 80
 ggc ttt ttg gtg agt att aac ggc gtg atg cat gtc att tac ccg cct 288
 Gly Phe Leu Val Ser Ile Asn Gly Val Met His Val Ile Tyr Pro Pro
 85 90 95
 aag cat att tta aag gat caa aac ggc tct aac ctc gtt ttt atc atg 336
 Lys His Ile Leu Lys Asp Gln Asn Gly Ser Asn Leu Val Phe Ile Met
 100 105 110
 cgc cat tta gag cgt gaa aaa atc tta aat tcc tta aag ggt ttt aag 384
 Arg His Leu Glu Arg Glu Lys Ile Leu Asn Ser Leu Lys Gly Phe Lys
 115 120 125
 gat ttt ctc ggc atc aag ggt ttt gaa acc caa 417
 Asp Phe Leu Gly Ile Lys Gly Phe Glu Thr Gln
 130 135
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 <212> PRT
 <213> Helicobacter pylori
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 Ser Ala Glu Ile Phe Asp Lys Arg Ala Ile Asp Tyr Glu Ser Leu Phe
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 20 25 30
 Ser His Ser Gln Gly Phe Glu Thr Leu Ser Ile Asn Phe Glu Gly Thr
 35 40 45
 Met Glu Trp Ser Ala Phe Gly Ile Trp Leu Ser Leu Leu His Gln
 50 55 60
 Tyr Gly Thr Gln Ile Leu Arg Ile Lys Gly Ile Ile Asp Ile Gly Ser
 65 70 75 80
 Gly Phe Leu Val Ser Ile Asn Gly Val Met His Val Ile Tyr Pro Pro
 85 90 95
 Lys His Ile Leu Lys Asp Gln Asn Gly Ser Asn Leu Val Phe Ile Met
 100 105 110
 Arg His Leu Glu Arg Glu Lys Ile Leu Asn Ser Leu Lys Gly Phe Lys
 115 120 125
 Asp Phe Leu Gly Ile Lys Gly Phe Glu Thr Gln
 130 135
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 <211> 615
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 <221> CDS
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 aaa gaa agc gct tta gaa tat tta aaa gcc aat ctc tct agc cag ttc 96
 Lys Glu Ser Ala Leu Glu Tyr Leu Lys Ala Asn Leu Ser Ser Gln Phe
 20 25 30
 ctt tac acg gaa atg ctg agc ttg aaa tta acc tat gaa agc gcc ctc 144
 Leu Tyr Thr Glu Met Leu Ser Leu Lys Leu Thr Tyr Glu Ser Ala Leu
 35 40 45
 caa caa gat tta aaa aag atc tta ggg gtt gaa gaa gtc att atg cta 192
 Gln Gln Asp Leu Lys Lys Ile Leu Gly Val Glu Glu Val Ile Met Leu
 50 55 60
 tcc aca agc ccc atg gaa tta cga tta gcc aat caa aag ctg ggc aat 240
 Ser Thr Ser Pro Met Glu Leu Arg Leu Ala Asn Gln Lys Leu Gly Asn
 65 70 75 80
 cgt ttc att aaa acc tta caa gcc atg aac gaa tta gac atg ggc gaa 288

Arg Phe Ile Lys Thr Leu Gln Ala Met Asn Glu Leu Asp Met Gly Glu
 85 90 95
 ttt ttt aac gct tac gct caa aaa acc aaa gat ccc acc cat gcc act 336
 Phe Phe Asn Ala Tyr Ala Gln Lys Thr Lys Asp Pro Thr His Ala Thr
 100 105 110
 agc tat ggc gtt ttt gcg gca agt ttg ggg att gaa ttg aaa aag gct 384
 Ser Tyr Gly Val Phe Ala Ala Ser Leu Gly Ile Glu Leu Lys Lys Ala
 115 120 125
 tta agg cat tat ctt tat gcg caa act tct aac atg gtg atc aac tgc 432
 Leu Arg His Tyr Leu Tyr Ala Gln Thr Ser Asn Met Val Ile Asn Cys
 130 135 140
 gtt aaa agc gtc cct tta tct caa aac gac ggg caa aaa atc tta ttg 480
 Val Lys Ser Val Pro Leu Ser Gln Asn Asp Gly Gln Lys Ile Leu Leu
 145 150 155 160
 agc ttg caa agc cct ttt aac cag ctc ata gaa aaa acc cta gaa cta 528
 Ser Leu Gln Ser Pro Phe Asn Gln Leu Ile Glu Lys Thr Leu Glu Leu
 165 170 175
 gac gaa agc cac ctg tgc acg gca agc gtt caa aac gac att aag gcg 576
 Asp Glu Ser His Leu Cys Thr Ala Ser Val Gln Asn Asp Ile Lys Ala
 180 185 190
 atg cag cat gag agt tta tac tcg cgc ctt tat atg tct 615
 Met Gln His Glu Ser Leu Tyr Ser Arg Leu Tyr Met Ser
 195 200 205

<210> 196

<211> 205

<212> PRT

<213> Helicobacter pylori

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 20 25 30
 Leu Tyr Thr Glu Met Leu Ser Leu Lys Leu Thr Tyr Glu Ser Ala Leu
 35 40 45
 Gln Gln Asp Leu Lys Lys Ile Leu Gly Val Glu Glu Val Ile Met Leu
 50 55 60
 Ser Thr Ser Pro Met Glu Leu Arg Leu Ala Asn Gln Lys Leu Gly Asn
 65 70 75 80
 Arg Phe Ile Lys Thr Leu Gln Ala Met Asn Glu Leu Asp Met Gly Glu
 85 90 95
 Phe Phe Asn Ala Tyr Ala Gln Lys Thr Lys Asp Pro Thr His Ala Thr
 100 105 110
 Ser Tyr Gly Val Phe Ala Ala Ser Leu Gly Ile Glu Leu Lys Lys Ala
 115 120 125
 Leu Arg His Tyr Leu Tyr Ala Gln Thr Ser Asn Met Val Ile Asn Cys
 130 135 140
 Val Lys Ser Val Pro Leu Ser Gln Asn Asp Gly Gln Lys Ile Leu Leu
 145 150 155 160
 Ser Leu Gln Ser Pro Phe Asn Gln Leu Ile Glu Lys Thr Leu Glu Leu
 165 170 175
 Asp Glu Ser His Leu Cys Thr Ala Ser Val Gln Asn Asp Ile Lys Ala
 180 185 190
 Met Gln His Glu Ser Leu Tyr Ser Arg Leu Tyr Met Ser
 195 200 205

<210> 197

<211> 1121

<212> DNA

<213> Helicobacter pylori

<220>

<221> CDS

<222> (1)..(1119)

<400> 197

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Pro Trp Ala Asn Gly Ser Ile Pro Lys Ser Asn Ser Thr Val Arg Phe	
1 5 10 15	
ggg ggg tat gag gga gtc aat tgg ggg aaa acg ggc tat att act ggc	96
Gly Gly Tyr Glu Gly Val Asn Trp Gly Lys Thr Gly Tyr Ile Thr Gly	
20 25 30	
act ttc aca gcc gat agg gtt tat atc acc ggt aac atg atg act ggt	144
Thr Phe Thr Ala Asp Arg Val Tyr Ile Thr Gly Asn Met Met Thr Gly	
35 40 45	
aac ggc gct caa acc ggt ggg ggg gcg act ttg aat ttt gtg ggc gcg	192
Asn Gly Ala Gln Thr Gly Gly Ala Thr Leu Asn Phe Val Gly Ala	
50 55 60	
act gaa att aat atc gct gga gcc act ttt aaa aac cta aaa acc act	240
Thr Glu Ile Asn Ile Ala Gly Ala Thr Phe Lys Asn Leu Lys Thr Thr	
65 70 75 80	
tca caa aac tct tac atg act ttt atg gca tta ggg gat agc tct ggg	288
Ser Gln Asn Ser Tyr Met Thr Phe Met Ala Leu Gly Asp Ser Ser Gly	
85 90 95	
agc gct aag atc aat gtt tct caa tct gat ttt tac gat tgg acg ggt	336
Ser Ala Lys Ile Asn Val Ser Gln Ser Asp Phe Tyr Asp Trp Thr Gly	
100 105 110	
ggg ggg tat gat ttt acc ggt aat ggc gtt ttt gat agc gtg aat ttc	384
Gly Gly Tyr Asp Phe Thr Gly Asn Gly Val Phe Asp Ser Val Asn Phe	
115 120 125	
aac aag gct tat tac aaa ttt caa ggc act gaa aat tct tac aat ttt	432
Asn Lys Ala Tyr Tyr Lys Phe Gln Gly Thr Glu Asn Ser Tyr Asn Phe	
130 135 140	
aaa aac acg aac ttt tta gca ggg aat ttt aag ttt cag ggc aag acc	480
Lys Asn Thr Asn Phe Leu Ala Gly Asn Phe Lys Phe Gln Gly Lys Thr	
145 150 155 160	
acc att gaa aaa tcc gtt tta agc gac gct tct tac act ttt gat ggc	528
Thr Ile Glu Lys Ser Val Leu Ser Asp Ala Ser Tyr Thr Phe Asp Gly	
165 170 175	
acg aat aac acc ttt act gaa gac aag ttt aat aat ggc tcg ttt aat	576
Thr Asn Asn Thr Phe Thr Glu Asp Lys Phe Asn Asn Gly Ser Phe Asn	
180 185 190	
ttt agt cat gca gag cag aca gac gct ttt aat aac aac tcg ttt aat	624
Phe Ser His Ala Glu Gln Thr Asp Ala Phe Asn Asn Asn Ser Phe Asn	
195 200 205	
ggc ggt tcg ttt agt ttt aac gcc aag caa gta aat ttt agt ggg aac	672
Gly Gly Ser Phe Ser Phe Asn Ala Lys Gln Val Asn Phe Ser Gly Asn	
210 215 220	
tcg ttc aat ggg ggc gtg ttt aat ttc aat aat acc cct aaa gtc agt	720
Ser Phe Asn Gly Gly Val Phe Asn Phe Asn Asn Thr Pro Lys Val Ser	
225 230 235 240	
ttc act gat gac act ttt aat gtg aat aac caa ttc aaa ata aat ggt	768
Phe Thr Asp Asp Thr Phe Asn Val Asn Asn Gln Phe Lys Ile Asn Gly	
245 250 255	
act caa aca act ttc act ttc aat aag ggc gtt gtt ttc aac atg caa	816
Thr Gln Thr Thr Phe Thr Phe Asn Lys Gly Val Val Phe Asn Met Gln	
260 265 270	
ggg ctt ttg agc agt tta agc gta ggc acg act tat caa ttg ctt aac	864
Gly Leu Leu Ser Ser Leu Ser Val Gly Thr Thr Tyr Gln Leu Leu Asn	
275 280 285	
gct aaa agc gtg gat tat aag gat aat aac gct ttg tat caa atg ctg	912
Ala Lys Ser Val Asp Tyr Lys Asp Asn Asn Ala Leu Tyr Gln Met Leu	
290 295 300	
cgt tgg att agt ggg gaa aac cct agc ggc acg cta gta aat aag gat	960
Arg Trp Ile Ser Gly Glu Asn Pro Ser Gly Thr Leu Val Asn Lys Asp	
305 310 315 320	

cag tcc gcg cca aac agc gct aaa att tat aat gtc cat ttc acc gat 1008
 Gln Ser Ala Pro Asn Ser Ala Lys Ile Tyr Asn Val His Phe Thr Asp
 325 330 335
 aac ggc ttg act tac tac atc aaa gaa aat ttt aat aat ggg atc acg 1056
 Asn Gly Leu Thr Tyr Tyr Ile Lys Glu Asn Phe Asn Asn Gly Ile Thr
 340 345 350
 ctc act cgt tta tgc act cta ggc tat acg cat tgc gtg aat att gat 1104
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 355 360 365
 aac gat gcg ttt aat ct 1121
 Asn Asp Ala Phe Asn
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 20 25 30
 Thr Phe Thr Ala Asp Arg Val Tyr Ile Thr Gly Asn Met Met Thr Gly
 35 40 45
 Asn Gly Ala Gln Thr Gly Gly Gly Ala Thr Leu Asn Phe Val Gly Ala
 50 55 60
 Thr Glu Ile Asn Ile Ala Gly Ala Thr Phe Lys Asn Leu Lys Thr Thr
 65 70 75 80
 Ser Gln Asn Ser Tyr Met Thr Phe Met Ala Leu Gly Asp Ser Ser Gly
 85 90 95
 Ser Ala Lys Ile Asn Val Ser Gln Ser Asp Phe Tyr Asp Trp Thr Gly
 100 105 110
 Gly Gly Tyr Asp Phe Thr Gly Asn Gly Val Phe Asp Ser Val Asn Phe
 115 120 125
 Asn Lys Ala Tyr Tyr Lys Phe Gln Gly Thr Glu Asn Ser Tyr Asn Phe
 130 135 140
 Lys Asn Thr Asn Phe Leu Ala Gly Asn Phe Lys Phe Gln Gly Lys Thr
 145 150 155 160
 Thr Ile Glu Lys Ser Val Leu Ser Asp Ala Ser Tyr Thr Phe Asp Gly
 165 170 175
 Thr Asn Asn Thr Phe Thr Glu Asp Lys Phe Asn Asn Gly Ser Phe Asn
 180 185 190
 Phe Ser His Ala Glu Gln Thr Asp Ala Phe Asn Asn Asn Ser Phe Asn
 195 200 205
 Gly Gly Ser Phe Ser Phe Asn Ala Lys Gln Val Asn Phe Ser Gly Asn
 210 215 220
 Ser Phe Asn Gly Gly Val Phe Asn Phe Asn Asn Thr Pro Lys Val Ser
 225 230 235 240
 Phe Thr Asp Asp Thr Phe Asn Val Asn Asn Gln Phe Lys Ile Asn Gly
 245 250 255
 Thr Gln Thr Thr Phe Thr Phe Asn Lys Gly Val Val Phe Asn Met Gln
 260 265 270
 Gly Leu Leu Ser Ser Leu Ser Val Gly Thr Thr Tyr Gln Leu Leu Asn
 275 280 285
 Ala Lys Ser Val Asp Tyr Lys Asp Asn Asn Ala Leu Tyr Gln Met Leu
 290 295 300
 Arg Trp Ile Ser Gly Glu Asn Pro Ser Gly Thr Leu Val Asn Lys Asp
 305 310 315 320
 Gln Ser Ala Pro Asn Ser Ala Lys Ile Tyr Asn Val His Phe Thr Asp
 325 330 335
 Asn Gly Leu Thr Tyr Tyr Ile Lys Glu Asn Phe Asn Asn Gly Ile Thr
 340 345 350

Leu Thr Arg Leu Cys Thr Leu Gly Tyr Thr His Cys Val Asn Ile Asp
 355 360 365

Asn Asp Ala Phe Asn
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<211> 679

<212> DNA

<213> Helicobacter pylori

<220>

<221> CDS

<222> (1)..(678)

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tta ctc aaa aaa atg gct aag gat tta aaa aat gcc ggg tta gcg caa	96
Leu Leu Lys Lys Met Ala Lys Asp Leu Lys Asn Ala Gly Leu Ala Gln	
20 25 30	
gtg aat gtt tca ttg gat tct tta aaa agc gat agg gtt tta aaa atc	144
Val Asn Val Ser Leu Asp Ser Leu Lys Ser Asp Arg Val Leu Lys Ile	
35 40 45	
tct caa aaa gac gct ctt aaa aac acg cta gaa ggg att gaa gag tct	192
Ser Gln Lys Asp Ala Leu Lys Asn Thr Leu Glu Gly Ile Glu Glu Ser	
50 55 60	
ttg aaa gtg ggt tta aaa ctc aaa tta aac acg gtt gtg ata aaa agc	240
Leu Lys Val Gly Leu Lys Leu Lys Leu Asn Thr Val Val Ile Lys Ser	
65 70 75 80	
gtt aat gat gat gaa atc tta gag ctt tta gaa tac gca aaa aat agg	288
Val Asn Asp Asp Glu Ile Leu Glu Leu Leu Glu Tyr Ala Lys Asn Arg	
85 90 95	
cat ata caa atc cgc tac att gaa ttt atg gaa aac acg cat gct aaa	336
His Ile Gln Ile Arg Tyr Ile Glu Phe Met Glu Asn Thr His Ala Lys	
100 105 110	
agt ttg gtt aaa ggc ttg aaa gag cga gaa att tta gat ttg atc gct	384
Ser Leu Val Lys Gly Leu Lys Glu Arg Glu Ile Leu Asp Leu Ile Ala	
115 120 125	
caa aaa tat caa atc att gag gca gaa aaa ccc aaa caa ggg tct tct	432
Gln Lys Tyr Gln Ile Ile Glu Ala Glu Lys Pro Lys Gln Gly Ser Ser	
130 135 140	
aaa atc tac acg cta gaa aat ggc tat caa ttt ggc att atc gct ccg	480
Lys Ile Tyr Thr Leu Glu Asn Gly Tyr Gln Phe Gly Ile Ile Ala Pro	
145 150 155 160	
cat agc gat gat ttt tgc caa tct tgc aat cgt atc cgt ttg gct tct	528
His Ser Asp Asp Phe Cys Gln Ser Cys Asn Arg Ile Arg Leu Ala Ser	
165 170 175	
gat ggt aag att tgc cca tgt tta tac tat caa gac gcc ata gac gct	576
Asp Gly Lys Ile Cys Pro Cys Leu Tyr Tyr Gln Asp Ala Ile Asp Ala	
180 185 190	
aaa gag gcg atc atc aat aag gat aca aaa aat ata aaa agg ctt tta	624
Lys Glu Ala Ile Ile Asn Lys Asp Thr Lys Asn Ile Lys Arg Leu Leu	
195 200 205	
aag caa tct gtc atc aat aaa cca gaa aaa aac atg tgg aat gat aaa	672
Lys Gln Ser Val Ile Asn Lys Pro Glu Lys Asn Met Trp Asn Asp Lys	
210 215 220	

aac agc g

Asn Ser

225

<210> 200

<211> 226

<212> PRT

<213> Helicobacter pylori

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 20 25 30
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 35 40 45
 Ser Gln Lys Asp Ala Leu Lys Asn Thr Leu Glu Gly Ile Glu Glu Ser
 50 55 60
 Leu Lys Val Gly Leu Lys Leu Lys Leu Asn Thr Val Val Ile Lys Ser
 65 70 75 80
 Val Asn Asp Asp Glu Ile Leu Glu Leu Leu Glu Tyr Ala Lys Asn Arg
 85 90 95
 His Ile Gln Ile Arg Tyr Ile Glu Phe Met Glu Asn Thr His Ala Lys
 100 105 110
 Ser Leu Val Lys Gly Leu Lys Glu Arg Glu Ile Leu Asp Leu Ile Ala
 115 120 125
 Gln Lys Tyr Gln Ile Ile Glu Ala Glu Lys Pro Lys Gln Gly Ser Ser
 130 135 140
 Lys Ile Tyr Thr Leu Glu Asn Gly Tyr Gln Phe Gly Ile Ile Ala Pro
 145 150 155 160
 His Ser Asp Asp Phe Cys Gln Ser Cys Asn Arg Ile Arg Leu Ala Ser
 165 170 175
 Asp Gly Lys Ile Cys Pro Cys Leu Tyr Tyr Gln Asp Ala Ile Asp Ala
 180 185 190
 Lys Glu Ala Ile Ile Asn Lys Asp Thr Lys Asn Ile Lys Arg Leu Leu
 195 200 205
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 210 215 220
 Asn Ser
 225

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<211> 486

<212> DNA

<213> Helicobacter pylori

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<221> CDS

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 1 5 10 15
 acc aac tct tta aaa atg act aaa caa gaa gtt aag gac gaa tac aaa 96
 Thr Asn Ser Leu Lys Met Thr Lys Gln Glu Val Lys Asp Glu Tyr Lys
 20 25 30
 cag caa gaa ggg aac cca gaa atc aaa gcc aaa atc cgc caa atg atg 144
 Gln Gln Glu Gly Asn Pro Glu Ile Lys Ala Lys Ile Arg Gln Met Met
 35 40 45
 cta aaa aac gcc acg aat aaa atg atg caa gaa atc cct aaa gcc aat 192
 Leu Lys Asn Ala Thr Asn Lys Met Met Gln Glu Ile Pro Lys Ala Asn
 50 55 60
 gtc gtg gtt act aac ccc acc cat tac gcc gtc gct ctc aaa ttt gat 240
 Val Val Val Thr Asn Pro Thr His Tyr Ala Val Ala Leu Lys Phe Asp
 65 70 75 80
 gaa gaa cac cct gtg cct gtg gta gtg gct aaa ggc acg gat tat tta 288
 Glu Glu His Pro Val Pro Val Val Val Ala Lys Gly Thr Asp Tyr Leu
 85 90 95
 gcc att agg att aag ggc atc gct aga gag cat gac ata gaa att ata 336
 Ala Ile Arg Ile Lys Gly Ile Ala Arg Glu His Asp Ile Glu Ile Ile
 100 105 110
 gaa aat aaa acg ctc gcc aga gag ctt tat aga gat gtg aaa tta aac 384

Glu Asn Lys Thr Leu Ala Arg Glu Leu Tyr Arg Asp Val Lys Leu Asn
 115 120 125
 gct gcc ata cca gaa gaa ttg ttt gaa gcc gtg gcg ata gtc ttc gct 432
 Ala Ala Ile Pro Glu Glu Leu Phe Glu Ala Val Ala Ile Val Phe Ala
 130 135 140
 caa gtg gct aaa tta gag caa gaa cgc caa aaa caa aag atc att aaa 480
 Gln Val Ala Lys Leu Glu Gln Glu Arg Gln Lys Gln Lys Ile Ile Lys
 145 150 155 160
 cct ctt 486
 Pro Leu
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 Phe Phe Val Leu Ala Phe Ile Asp Leu Ala Ile Lys Arg Arg Gln Tyr
 1 5 10 15
 Thr Asn Ser Leu Lys Met Thr Lys Gln Glu Val Lys Asp Glu Tyr Lys
 20 25 30
 Gln Gln Glu Gly Asn Pro Glu Ile Lys Ala Lys Ile Arg Gln Met Met
 35 40 45
 Leu Lys Asn Ala Thr Asn Lys Met Met Gln Glu Ile Pro Lys Ala Asn
 50 55 60
 Val Val Val Thr Asn Pro Thr His Tyr Ala Val Ala Leu Lys Phe Asp
 65 70 75 80
 Glu Glu His Pro Val Pro Val Val Val Ala Lys Gly Thr Asp Tyr Leu
 85 90 95
 Ala Ile Arg Ile Lys Gly Ile Ala Arg Glu His Asp Ile Glu Ile Ile
 100 105 110
 Glu Asn Lys Thr Leu Ala Arg Glu Leu Tyr Arg Asp Val Lys Leu Asn
 115 120 125
 Ala Ala Ile Pro Glu Glu Leu Phe Glu Ala Val Ala Ile Val Phe Ala
 130 135 140
 Gln Val Ala Lys Leu Glu Gln Glu Arg Gln Lys Gln Lys Ile Ile Lys
 145 150 155 160
 Pro Leu
 <210> 203
 <211> 174
 <212> DNA
 <213> Helicobacter pylori
 <220>
 <221> CDS
 <222> (1)..(174)
 <400> 203
 acc gga aga acc cat caa atc aga gtc cat tta aag cat atc aac cac 48
 Thr Gly Arg Thr His Gln Ile Arg Val His Leu Lys His Ile Asn His
 1 5 10 15
 ccc att ata ggc gat acg ctt tat aat aac gag cca agt tta gcc aaa 96
 Pro Ile Ile Gly Asp Thr Leu Tyr Asn Asn Glu Pro Ser Leu Ala Lys
 20 25 30
 cgc ttg atg ctc cat gca cat aaa atc gcg cta cta ggg tat gaa ttt 144
 Arg Leu Met Leu His Ala His Lys Ile Ala Leu Leu Gly Tyr Glu Phe
 35 40 45
 gaa gcg atc gct cct aaa gaa ttt gaa att 174
 Glu Ala Ile Ala Pro Lys Glu Phe Glu Ile
 50 55
 <210> 204
 <211> 58
 <212> PRT
 <213> Helicobacter pylori

<400> 204

Thr Gly Arg Thr His Gln Ile Arg Val His Leu Lys His Ile Asn His
 1 5 10 15
 Pro Ile Ile Gly Asp Thr Leu Tyr Asn Asn Glu Pro Ser Leu Ala Lys
 20 25 30
 Arg Leu Met Leu His Ala His Lys Ile Ala Leu Leu Gly Tyr Glu Phe
 35 40 45
 Glu Ala Ile Ala Pro Lys Glu Phe Glu Ile
 50 55

<210> 205

<211> 69

<212> DNA

<213> Helicobacter pylori

<220>

<221> CDS

<222> (1)..(69)

<400> 205

caa gaa atg cac att ctt atg atc cac atc tta tgc gat tgc att gaa 48
 Gln Glu Met His Ile Leu Met Ile His Ile Leu Cys Asp Cys Ile Glu
 1 5 10 15
 agg cat ttc gct cat aaa aat 69
 Arg His Phe Ala His Lys Asn
 20

<210> 206

<211> 23

<212> PRT

<213> Helicobacter pylori

<400> 206

Gln Glu Met His Ile Leu Met Ile His Ile Leu Cys Asp Cys Ile Glu
 1 5 10 15
 Arg His Phe Ala His Lys Asn
 20

<210> 207

<211> 423

<212> DNA

<213> Helicobacter pylori

<220>

<221> CDS

<222> (1)..(423)

<400> 207

agg cat tat gaa acg atg ttt att ctc aaa cct act tta gta gaa gaa 48
 Arg His Tyr Glu Thr Met Phe Ile Leu Lys Pro Thr Leu Val Glu Glu
 1 5 10 15
 gag att aaa tcc aag att gag ttt tat aaa gaa gtg atc act aag cat 96
 Glu Ile Lys Ser Lys Ile Glu Phe Tyr Lys Glu Val Ile Thr Lys His
 20 25 30
 cac ggc gtg att gaa acg agc ctg gat atg ggc atg cgt aat tta gct 144
 His Gly Val Ile Glu Thr Ser Leu Asp Met Gly Met Arg Asn Leu Ala
 35 40 45
 tat gaa atc aaa aag cac aaa aga ggc tat tat tat gtg gcg tat ttc 192
 Tyr Glu Ile Lys Lys His Lys Arg Gly Tyr Tyr Tyr Val Ala Tyr Phe
 50 55 60
 aaa gcg gag ccg tca atg att gta gag ctt gaa cga ttg tat cgc atc 240
 Lys Ala Glu Pro Ser Met Ile Val Glu Leu Glu Arg Leu Tyr Arg Ile
 65 70 75 80
 aat gaa gac gtg ttg cgt ttc att gtg atc aaa tac gaa agc aag aaa 288
 Asn Glu Asp Val Leu Arg Phe Ile Val Ile Lys Tyr Glu Ser Lys Lys
 85 90 95
 gaa gtg gaa gcg tgg cat gcg ttg gtg gat agg gct aat aaa aag cca 336
 Glu Val Glu Ala Trp His Ala Leu Val Asp Arg Ala Asn Lys Lys Pro
 100 105 110

tcg cac gcc aaa gaa aaa cac gaa aaa acc gaa cac acg cat tct cac	384
Ser His Ala Lys Glu Lys His Glu Lys Thr Glu His Thr His Ser His	
115 120 125	
cac aca gag gaa gca gaa agc gta gga tct cat agc gaa	423
His Thr Glu Glu Ala Glu Ser Val Gly Ser His Ser Glu	
130 135 140	
<210> 208	
<211> 141	
<212> PRT	
<213> Helicobacter pylori	
<400> 208	
Arg His Tyr Glu Thr Met Phe Ile Leu Lys Pro Thr Leu Val Glu Glu	
1 5 10 15	
Glu Ile Lys Ser Lys Ile Glu Phe Tyr Lys Glu Val Ile Thr Lys His	
20 25 30	
His Gly Val Ile Glu Thr Ser Leu Asp Met Gly Met Arg Asn Leu Ala	
35 40 45	
Tyr Glu Ile Lys Lys His Lys Arg Gly Tyr Tyr Tyr Val Ala Tyr Phe	
50 55 60	
Lys Ala Glu Pro Ser Met Ile Val Glu Leu Glu Arg Leu Tyr Arg Ile	
65 70 75 80	
Asn Glu Asp Val Leu Arg Phe Ile Val Ile Lys Tyr Glu Ser Lys Lys	
85 90 95	
Glu Val Glu Ala Trp His Ala Leu Val Asp Arg Ala Asn Lys Lys Pro	
100 105 110	
Ser His Ala Lys Glu Lys His Glu Lys Thr Glu His Thr His Ser His	
115 120 125	
His Thr Glu Glu Ala Glu Ser Val Gly Ser His Ser Glu	
130 135 140	
<210> 209	
<211> 212	
<212> DNA	
<213> Helicobacter pylori	
<220>	
<221> CDS	
<222> (1)... (210)	
<400> 209	
tca agc gat aac ccg cta gcc gat gag ccg gat ttg gat tac gct aac	48
Ser Ser Asp Asn Pro Leu Ala Asp Glu Pro Asp Leu Asp Tyr Ala Asn	
1 5 10 15	
atg agc gct gaa gaa gtg gaa gca gag att gaa cgg ctg ctg aac aaa	96
Met Ser Ala Glu Glu Val Glu Ala Glu Ile Glu Arg Leu Leu Asn Lys	
20 25 30	
cgc caa gaa gcc gat aaa gaa cga aga gct caa aaa aaa caa gaa gcc	144
Arg Gln Glu Ala Asp Lys Glu Arg Arg Ala Gln Lys Lys Gln Glu Ala	
35 40 45	
aaa ccc aaa caa gaa gtt acc cca aca aaa gaa acc ccc aaa gcc cct	192
Lys Pro Lys Gln Glu Val Thr Pro Thr Lys Glu Thr Pro Lys Ala Pro	
50 55 60	
aaa acc gaa act aaa gct aa	212
Lys Thr Glu Thr Lys Ala	
65 70	
<210> 210	
<211> 70	
<212> PRT	
<213> Helicobacter pylori	
<400> 210	
Ser Ser Asp Asn Pro Leu Ala Asp Glu Pro Asp Leu Asp Tyr Ala Asn	
1 5 10 15	
Met Ser Ala Glu Glu Val Glu Ala Glu Ile Glu Arg Leu Leu Asn Lys	
20 25 30	

Arg Gln Glu Ala Asp Lys Glu Arg Arg Ala Gln Lys Lys Gln Glu Ala
 35 40 45
 Lys Pro Lys Gln Glu Val Thr Pro Thr Lys Glu Thr Pro Lys Ala Pro
 50 55 60
 Lys Thr Glu Thr Lys Ala
 65 70

<210> 211

<211> 798

<212> DNA

<213> Helicobacter pylori

<220>

<221> CDS

<222> (1)..(798)

<400> 211

gca gaa gaa agt aaa ggg agt gtt gca aaa tat aaa ata gaa gct caa	48
Ala Glu Glu Ser Lys Gly Ser Val Ala Lys Tyr Lys Ile Glu Ala Gln	
1 5 10 15	
tac agc att gat ttt gat tct gca gaa cac act tca ctt ttc att ccc	96
Tyr Ser Ile Asp Phe Asp Ser Ala Glu His Thr Ser Leu Phe Ile Pro	
20 25 30	
atg ccg agt gtt gta gcg agc aat gtg cat tta caa ggc aat cat gct	144
Met Pro Ser Val Val Ala Ser Asn Val His Leu Gln Gly Asn His Ala	
35 40 45	
agc tat aaa agc atg ctc aat ttt gga gtg cct tat ttg caa gtg gat	192
Ser Tyr Lys Ser Met Leu Asn Phe Gly Val Pro Tyr Leu Gln Val Asp	
50 55 60	
ttt tta aaa agc act caa aaa aag caa gtc cat ttg tct tat gag atc	240
Phe Leu Lys Ser Thr Gln Lys Lys Gln Val His Leu Ser Tyr Glu Ile	
65 70 75 80	
gct agc tat caa ttg aat gag cgt ttg ttt gaa acg agc gat ttt gta	288
Ala Ser Tyr Gln Leu Asn Glu Arg Leu Phe Glu Thr Ser Asp Phe Val	
85 90 95	
gca atg ggg cgt tat gaa aga gac gat gcg agc gtg gct aac att gcc	336
Ala Met Gly Arg Tyr Glu Arg Asp Asp Ala Ser Val Ala Asn Ile Ala	
100 105 110	
aac cag ctt aag gga aca acc cct aaa gaa agc gtt cgc aat ttt tat	384
Asn Gln Leu Lys Gly Thr Thr Pro Lys Glu Ser Val Arg Asn Phe Tyr	
115 120 125	
gcg ttc atc aag cat gag atg cct aag aga cag aag gct tta gag ggt	432
Ala Phe Ile Lys His Glu Met Pro Lys Arg Gln Lys Ala Leu Glu Gly	
130 135 140	
aaa gaa aat tta cct aag cgt gag agt ttg ccc tgg ttt gca acc att	480
Lys Glu Asn Leu Pro Lys Arg Glu Ser Leu Pro Trp Phe Ala Thr Ile	
145 150 155 160	
tca aaa gag agc atg ttt gtg tcc tta tgc cat gcg tgc ggg att aaa	528
Ser Lys Glu Ser Met Phe Val Ser Leu Cys His Ala Cys Gly Ile Lys	
165 170 175	
agc gct gaa gtg caa ggc ttg aaa ctg ggt caa aac agc gtg gtg aaa	576
Ser Ala Glu Val Gln Gly Leu Lys Leu Gly Gln Asn Ser Val Val Lys	
180 185 190	
aac gct cct aga gtg gaa gtg tat ttg aaa gat tca ttt cta gcg ttt	624
Asn Ala Pro Arg Val Glu Val Tyr Leu Lys Asp Ser Phe Leu Ala Phe	
195 200 205	
gat ttt caa aat aat cac aag gaa gtt ttt atc ccg ttg aat cgt cat	672
Asp Phe Gln Asn Asn His Lys Glu Val Phe Ile Pro Leu Asn Arg His	
210 215 220	
aaa gac atg cag tta gat tct gcc tta ttg gcg act ttt ggc gat gct	720
Lys Asp Met Gln Leu Asp Ser Ala Leu Leu Ala Thr Phe Gly Asp Ala	
225 230 235 240	
ttt gcc ctt gtg gat ggt agg gat tta ggc aat tac gag agc aaa ctt	768
Phe Ala Leu Val Asp Gly Arg Asp Leu Gly Asn Tyr Glu Ser Lys Leu	

245 250 255 798
 ttt gaa aaa aga gtg tcc tat acg att gtc
 Phe Glu Lys Arg Val Ser Tyr Thr Ile Val
 260 265

<210> 212

<211> 266

<212> PRT

<213> Helicobacter pylori

<400> 212

Ala Glu Glu Ser Lys Gly Ser Val Ala Lys Tyr Lys Ile Glu Ala Gln
 1 5 10 15
 Tyr Ser Ile Asp Phe Asp Ser Ala Glu His Thr Ser Leu Phe Ile Pro
 20 25 30
 Met Pro Ser Val Val Ala Ser Asn Val His Leu Gln Gly Asn His Ala
 35 40 45
 Ser Tyr Lys Ser Met Leu Asn Phe Gly Val Pro Tyr Leu Gln Val Asp
 50 55 60
 Phe Leu Lys Ser Thr Gln Lys Lys Gln Val His Leu Ser Tyr Glu Ile
 65 70 75 80
 Ala Ser Tyr Gln Leu Asn Glu Arg Leu Phe Glu Thr Ser Asp Phe Val
 85 90 95
 Ala Met Gly Arg Tyr Glu Arg Asp Asp Ala Ser Val Ala Asn Ile Ala
 100 105 110
 Asn Gln Leu Lys Gly Thr Thr Pro Lys Glu Ser Val Arg Asn Phe Tyr
 115 120 125
 Ala Phe Ile Lys His Glu Met Pro Lys Arg Gln Lys Ala Leu Glu Gly
 130 135 140
 Lys Glu Asn Leu Pro Lys Arg Glu Ser Leu Pro Trp Phe Ala Thr Ile
 145 150 155 160
 Ser Lys Glu Ser Met Phe Val Ser Leu Cys His Ala Cys Gly Ile Lys
 165 170 175
 Ser Ala Glu Val Gln Gly Leu Lys Leu Gly Gln Asn Ser Val Val Lys
 180 185 190
 Asn Ala Pro Arg Val Glu Val Tyr Leu Lys Asp Ser Phe Leu Ala Phe
 195 200 205
 Asp Phe Gln Asn Asn His Lys Glu Val Phe Ile Pro Leu Asn Arg His
 210 215 220
 Lys Asp Met Gln Leu Asp Ser Ala Leu Leu Ala Thr Phe Gly Asp Ala
 225 230 235 240
 Phe Ala Leu Val Asp Gly Arg Asp Leu Gly Asn Tyr Glu Ser Lys Leu
 245 250 255
 Phe Glu Lys Arg Val Ser Tyr Thr Ile Val
 260 265

<210> 213

<211> 170

<212> DNA

<213> Helicobacter pylori

<220>

<221> CDS

<222> (1)..(168)

<400> 213

tgc atg ttt gat ggc tat acg cat tat ttg aat ttg gtg ctt gtc aat 48
 Cys Met Phe Asp Gly Tyr Thr His Tyr Leu Asn Leu Val Leu Val Asn
 1 5 10 15
 tgc ccc ata gag ctc tct ggt gtg cga gaa tgc att gaa gaa agc gaa 96
 Cys Pro Ile Glu Leu Ser Gly Val Arg Glu Cys Ile Glu Glu Ser Glu
 20 25 30
 ggg gtg gat ggg gca gtg agt gaa acc gct agt tct cat tta tgc gtg 144
 Gly Val Asp Gly Ala Val Ser Glu Thr Ala Ser Ser His Leu Cys Val
 35 40 45
 aaa gct tta gcg aaa ggc tca gaa cc 170

Lys Ala Leu Ala Lys Gly Ser Glu
50 55

<210> 214

<211> 56

<212> PRT

<213> Helicobacter pylori

<400> 214

Cys Met Phe Asp Gly Tyr Thr His Tyr Leu Asn Leu Val Leu Val Asn
1 5 10 15

Cys Pro Ile Glu Leu Ser Gly Val Arg Glu Cys Ile Glu Glu Ser Glu
20 25 30

Gly Val Asp Gly Ala Val Ser Glu Thr Ala Ser Ser His Leu Cys Val
35 40 45

Lys Ala Leu Ala Lys Gly Ser Glu
50 55

<210> 215

<211> 717

<212> DNA

<213> Helicobacter pylori

<220>

<221> CDS

<222> (1)..(717)

<400> 215

ggc ggc att gcg tgc gcg aat ttg ttg cat aaa aat tca ggc atc acg 48

Gly Gly Ile Ala Cys Ala Asn Leu Leu His Lys Asn Ser Gly Ile Thr
1 5 10 15

ata gat att gga ggc ggt agc acc gag tgc gcg ttg att gaa aaa ggc 96

Ile Asp Ile Gly Gly Gly Ser Thr Glu Cys Ala Leu Ile Glu Lys Gly
20 25 30

aag att aag gac tta atc tcg ctt gat gtt ggc acg att cgc att aaa 144

Lys Ile Lys Asp Leu Ile Ser Leu Asp Val Gly Thr Ile Arg Ile Lys
35 40 45

gaa atg ttt tta gac aaa gac tta gag gtc aaa ttg gct aaa gcc ttt 192

Glu Met Phe Leu Asp Lys Asp Leu Glu Val Lys Leu Ala Lys Ala Phe
50 55 60

atc caa aaa gaa gtc tct aaa ctg ccc ttt aaa cac aaa aac gcc ttt 240

Ile Gln Lys Glu Val Ser Lys Leu Pro Phe Lys His Lys Asn Ala Phe
65 70 75 80

ggg gtg ggc ggc acg atc aga gcg ttg agt aag gta ttg atg aaa cgc 288

Gly Val Gly Gly Thr Ile Arg Ala Leu Ser Lys Val Leu Met Lys Arg
85 90 95

ttt tgt tac cct att gat tct ttg cat ggc tat gaa ata gat gca cat 336

Phe Cys Tyr Pro Ile Asp Ser Leu His Gly Tyr Glu Ile Asp Ala His
100 105 110

aaa aat tta gcg ttc att gaa aaa atc gtc atg ctc aaa gaa gat caa 384

Lys Asn Leu Ala Phe Ile Glu Lys Ile Val Met Leu Lys Glu Asp Gln
115 120 125

tta cgg ctt tta ggc gtg aat gaa gag cgt ttg gat agc atc agg agc 432

Leu Arg Leu Leu Gly Val Asn Glu Glu Arg Leu Asp Ser Ile Arg Ser
130 135 140

ggg gcg ttg att tta tca gtc gtt ttg gag cat tta aaa act tct tta 480

Gly Ala Leu Ile Leu Ser Val Val Leu Glu His Leu Lys Thr Ser Leu
145 150 155 160

atg atc act agt ggc gtg ggc gtg aga gaa ggc gtg ttt ttg agc gat 528

Met Ile Thr Ser Gly Val Gly Val Arg Glu Gly Val Phe Leu Ser Asp
165 170 175

tta ttg cgc cat cat tac cat aaa ttc ccc ccc aat atc aac ccc tct 576

Leu Leu Arg His His Tyr His Lys Phe Pro Pro Asn Ile Asn Pro Ser
180 185 190

ctc atc tct tta aaa gat cgc ttt ttg ccc cat gaa aag cac agc caa 624

Leu Ile Ser Leu Lys Asp Arg Phe Leu Pro His Glu Lys His Ser Gln

195 200 205
 aag gtc aaa aaa gaa tgc gtg aaa ttg ttt gaa gcc tta tcg cct ttg 672
 Lys Val Lys Lys Glu Cys Val Lys Leu Phe Glu Ala Leu Ser Pro Leu
 210 215 220
 cat aaa ata gat gaa aaa tac ctt ttc cat tta aag att gcg ggg 717
 His Lys Ile Asp Glu Lys Tyr Leu Phe His Leu Lys Ile Ala Gly
 225 230 235
 <210> 216
 <211> 239
 <212> PRT
 <213> *Helicobacter pylori*
 <400> 216
 Gly Gly Ile Ala Cys Ala Asn Leu Leu His Lys Asn Ser Gly Ile Thr
 1 5 10 15
 Ile Asp Ile Gly Gly Gly Ser Thr Glu Cys Ala Leu Ile Glu Lys Gly
 20 25 30
 Lys Ile Lys Asp Leu Ile Ser Leu Asp Val Gly Thr Ile Arg Ile Lys
 35 40 45
 Glu Met Phe Leu Asp Lys Asp Leu Glu Val Lys Leu Ala Lys Ala Phe
 50 55 60
 Ile Gln Lys Glu Val Ser Lys Leu Pro Phe Lys His Lys Asn Ala Phe
 65 70 75 80
 Gly Val Gly Gly Thr Ile Arg Ala Leu Ser Lys Val Leu Met Lys Arg
 85 90 95
 Phe Cys Tyr Pro Ile Asp Ser Leu His Gly Tyr Glu Ile Asp Ala His
 100 105 110
 Lys Asn Leu Ala Phe Ile Glu Lys Ile Val Met Leu Lys Glu Asp Gln
 115 120 125
 Leu Arg Leu Leu Gly Val Asn Glu Glu Arg Leu Asp Ser Ile Arg Ser
 130 135 140
 Gly Ala Leu Ile Leu Ser Val Val Leu Glu His Leu Lys Thr Ser Leu
 145 150 155 160
 Met Ile Thr Ser Gly Val Gly Val Arg Glu Gly Val Phe Leu Ser Asp
 165 170 175
 Leu Leu Arg His His Tyr His Lys Phe Pro Pro Asn Ile Asn Pro Ser
 180 185 190
 Leu Ile Ser Leu Lys Asp Arg Phe Leu Pro His Glu Lys His Ser Gln
 195 200 205
 Lys Val Lys Lys Glu Cys Val Lys Leu Phe Glu Ala Leu Ser Pro Leu
 210 215 220
 His Lys Ile Asp Glu Lys Tyr Leu Phe His Leu Lys Ile Ala Gly
 225 230 235
 <210> 217
 <211> 480
 <212> DNA
 <213> *Helicobacter pylori*
 <220>
 <221> CDS
 <222> (1)..(480)
 <400> 217
 tct tct tta caa agc gaa cac atc aat tcc ccc ctt gtc cca gaa gcg 48
 Ser Ser Leu Gln Ser Glu His Ile Asn Ser Pro Leu Val Pro Glu Ala
 1 5 10 15
 atg cta gct tta ggg caa gcg cac atg aaa aag aaa gag tat gtt tta 96
 Met Leu Ala Leu Gly Gln Ala His Met Lys Lys Lys Glu Tyr Val Leu
 20 25 30
 gcg tct ttt tac ttt gat gaa tac atc aag cgc ttt ggg act aag gac 144
 Ala Ser Phe Tyr Phe Asp Glu Tyr Ile Lys Arg Phe Gly Thr Lys Asp
 35 40 45
 aat gtg gat tat ttg act ttt tta aaa ttg caa tcg cat tat tac gct 192
 Asn Val Asp Tyr Leu Thr Phe Leu Lys Leu Gln Ser His Tyr Tyr Ala

50	55	60	
ttc aaa aac cat tct aaa gac cag gaa ttt atc tct aat tct att gtg			240
Phe Lys Asn His Ser Lys Asp Gln Glu Phe Ile Ser Asn Ser Ile Val			
65	70	75	80
agt tta ggc gaa ttt ata gaa aaa tac cct aac agc cgt tac cgc ccc			288
Ser Leu Gly Glu Phe Ile Glu Lys Tyr Pro Asn Ser Arg Tyr Arg Pro			
85	90	95	
tat gta gaa tac atg caa atc aaa ttc att tta ggg caa aat gag ctc			336
Tyr Val Glu Tyr Met Gln Ile Lys Phe Ile Leu Gly Gln Asn Glu Leu			
100	105	110	
aat cgc gcg atc gcg aat gtc tat aaa aaa cgc cac aag cct gag ggc			384
Asn Arg Ala Ile Ala Asn Val Tyr Lys Lys Arg His Lys Pro Glu Gly			
115	120	125	
gtg aaa cgc tat tta gaa agg ata gat gag act tta gaa aaa gag act			432
Val Lys Arg Tyr Leu Glu Arg Ile Asp Glu Thr Leu Glu Lys Glu Thr			
130	135	140	
aaa ccc aaa cca tcg cac atg cct tgg tat gtg tta att ttt gat tgg			480
Lys Pro Lys Pro Ser His Met Pro Trp Tyr Val Leu Ile Phe Asp Trp			
145	150	155	160

<210> 218

<211> 160

<212> PRT

<213> Helicobacter pylori

<400> 218

Ser Ser Leu Gln Ser Glu His Ile Asn Ser Pro Leu Val Pro Glu Ala	
1	15
Met Leu Ala Leu Gly Gln Ala His Met Lys Lys Lys Glu Tyr Val Leu	
20	30
Ala Ser Phe Tyr Phe Asp Glu Tyr Ile Lys Arg Phe Gly Thr Lys Asp	
35	45
Asn Val Asp Tyr Leu Thr Phe Leu Lys Leu Gln Ser His Tyr Tyr Ala	
50	60
Phe Lys Asn His Ser Lys Asp Gln Glu Phe Ile Ser Asn Ser Ile Val	
65	80
Ser Leu Gly Glu Phe Ile Glu Lys Tyr Pro Asn Ser Arg Tyr Arg Pro	
85	95
Tyr Val Glu Tyr Met Gln Ile Lys Phe Ile Leu Gly Gln Asn Glu Leu	
100	110
Asn Arg Ala Ile Ala Asn Val Tyr Lys Lys Arg His Lys Pro Glu Gly	
115	125
Val Lys Arg Tyr Leu Glu Arg Ile Asp Glu Thr Leu Glu Lys Glu Thr	
130	140
Lys Pro Lys Pro Ser His Met Pro Trp Tyr Val Leu Ile Phe Asp Trp	
145	160

<210> 219

<211> 814

<212> DNA

<213> Helicobacter pylori

<220>

<221> CDS

<222> (1)..(813)

<400> 219

gac agc aaa aaa gac gct tgc ggg ttc atc tat gag atc agc gag ttc	48
Asp Ser Lys Lys Asp Ala Cys Gly Phe Ile Tyr Glu Ile Ser Glu Phe	
1	15
atg aaa gcc tat acc gca ttg cta aaa aaa gac cga tac gtc tat	96
Met Lys Ala Tyr Thr Ala Leu Leu Lys Lys Gln Asp Arg Tyr Val Tyr	
20	30
tta ttg agg tat ctc ccc tct agg tat tgg gcc agc att tta acg act	144
Leu Leu Arg Tyr Leu Pro Ser Arg Tyr Trp Ala Ser Ile Leu Thr Thr	
35	45

gcc ctt tat gtc aaa tac cct gat ttt gac gct ttg aaa aag ctt ttg 192
 Ala Leu Tyr Val Lys Tyr Pro Asp Phe Asp Ala Leu Lys Lys Leu Leu
 50 55 60
 gtg tct tat tat tac caa act tgg att gca gga ggc acg atc acg cgc 240
 Val Ser Tyr Tyr Tyr Gln Thr Trp Ile Ala Gly Gly Thr Ile Thr Arg
 65 70 75 80
 atc aag caa acc agt atc aac att atc aaa aac gtt aaa agc aat aag 288
 Ile Lys Gln Thr Ser Ile Asn Ile Ile Lys Asn Val Lys Ser Asn Lys
 85 90 95
 agc gtt gaa acc atc aaa gag ctt ata ttg aat agc atc gac tct tat 336
 Ser Val Glu Thr Ile Lys Glu Leu Ile Leu Asn Ser Ile Asp Ser Tyr
 100 105 110
 aac acc ttt gat caa tac ctc tat aac tta tgg gat agc tct tct gtt 384
 Asn Thr Phe Asp Gln Tyr Leu Tyr Asn Leu Trp Asp Ser Ser Val
 115 120 125
 tat cat agc aaa tgg gtg cgt cct gtc tta gcc cta gct aat tat ttc 432
 Tyr His Ser Lys Trp Val Arg Pro Val Leu Ala Leu Ala Asn Tyr Phe
 130 135 140
 atg gca gat gaa gag aaa ccc cat ttt atc gct atg gat gcc gaa acc 480
 Met Ala Asp Glu Glu Lys Pro His Phe Ile Ala Met Asp Ala Glu Thr
 145 150 155 160
 caa gtg gag cat att ttg cca caa acg ccc aaa aga ggc agt caa tgg 528
 Gln Val Glu His Ile Leu Pro Gln Thr Pro Lys Arg Gly Ser Gln Trp
 165 170 175
 aac gcg gat ttt gac aaa gaa aaa aga gaa gaa tgg gta aat aat atc 576
 Asn Ala Asp Phe Asp Lys Glu Lys Arg Glu Glu Trp Val Asn Asn Ile
 180 185 190
 gcg aat tta acc ctt tta aag cgt aaa aag aac gcg cat gct tta aac 624
 Ala Asn Leu Thr Leu Leu Lys Arg Lys Lys Asn Ala His Ala Leu Asn
 195 200 205
 ggg gat ttt gat gaa aaa aga aaa att tat gga ggc aaa gac acg agc 672
 Gly Asp Phe Asp Glu Lys Arg Lys Ile Tyr Gly Gly Lys Asp Thr Ser
 210 215 220
 aaa gtg att agc tgt tat gac atc act aaa gaa ttg tat agc aat tat 720
 Lys Val Ile Ser Cys Tyr Asp Ile Thr Lys Glu Leu Tyr Ser Asn Tyr
 225 230 235 240
 agg aag tgg aat gag aag tcc ctc caa gag cga tac aaa tct ttg tat 768
 Arg Lys Trp Asn Glu Lys Ser Leu Gln Glu Arg Tyr Lys Ser Leu Tyr
 245 250 255
 aac act atc acg cct gtt tta cac ata gag ggg caa gaa gat gat t 814
 Asn Thr Ile Thr Pro Val Leu His Ile Glu Gly Gln Glu Asp Asp
 260 265 270

<210> 220

<211> 271

<212> PRT

<213> Helicobacter pylori

<400> 220

Asp Ser Lys Lys Asp Ala Cys Gly Phe Ile Tyr Glu Ile Ser Glu Phe
 1 5 10 15
 Met Lys Ala Tyr Thr Ala Leu Leu Lys Lys Gln Asp Arg Tyr Val Tyr
 20 25 30
 Leu Leu Arg Tyr Leu Pro Ser Arg Tyr Trp Ala Ser Ile Leu Thr Thr
 35 40 45
 Ala Leu Tyr Val Lys Tyr Pro Asp Phe Asp Ala Leu Lys Lys Leu Leu
 50 55 60
 Val Ser Tyr Tyr Tyr Gln Thr Trp Ile Ala Gly Gly Thr Ile Thr Arg
 65 70 75 80
 Ile Lys Gln Thr Ser Ile Asn Ile Ile Lys Asn Val Lys Ser Asn Lys
 85 90 95
 Ser Val Glu Thr Ile Lys Glu Leu Ile Leu Asn Ser Ile Asp Ser Tyr
 100 105 110

Asn Thr Phe Asp Gln Tyr Leu Tyr Asn Leu Trp Asp Ser Ser Ser Val
 115 120 125
 Tyr His Ser Lys Trp Val Arg Pro Val Leu Ala Leu Ala Asn Tyr Phe
 130 135 140
 Met Ala Asp Glu Glu Lys Pro His Phe Ile Ala Met Asp Ala Glu Thr
 145 150 155 160
 Gln Val Glu His Ile Leu Pro Gln Thr Pro Lys Arg Gly Ser Gln Trp
 165 170 175
 Asn Ala Asp Phe Asp Lys Glu Lys Arg Glu Glu Trp Val Asn Asn Ile
 180 185 190
 Ala Asn Leu Thr Leu Leu Lys Arg Lys Lys Asn Ala His Ala Leu Asn
 195 200 205
 Gly Asp Phe Asp Glu Lys Arg Lys Ile Tyr Gly Gly Lys Asp Thr Ser
 210 215 220
 Lys Val Ile Ser Cys Tyr Asp Ile Thr Lys Glu Leu Tyr Ser Asn Tyr
 225 230 235 240
 Arg Lys Trp Asn Glu Lys Ser Leu Gln Glu Arg Tyr Lys Ser Leu Tyr
 245 250 255
 Asn Thr Ile Thr Pro Val Leu His Ile Glu Gly Gln Glu Asp Asp
 260 265 270

<210> 221

<211> 648

<212> DNA

<213> Helicobacter pylori

<220>

<221> CDS

<222> (1)..(648)

<400> 221

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 Lys Tyr Ile Asn Ser Pro Gln Ser Lys Leu Phe Asp Lys Ser Ser Leu
 1 5 10 15
 ctc tat ggc tat cat ttg gct aaa gaa cac atc tat aaa caa aag caa 96
 Leu Tyr Gly Tyr His Leu Ala Lys Glu His Ile Tyr Lys Gln Lys Gln
 20 25 30
 gtc att gta aca gag ggg tat ttg gat gtg att tta ttg cac cag gcg 144
 Val Ile Val Thr Glu Gly Tyr Leu Asp Val Ile Leu Leu His Gln Ala
 35 40 45
 ggt ttt aaa aac gcc ata gcc acg ctt ggg aca gct tta acg cca tcg 192
 Gly Phe Lys Asn Ala Ile Ala Thr Leu Gly Thr Ala Leu Thr Pro Ser
 50 55 60
 cat ttg ccc ttg ctt aaa aaa ggc gat ccc gaa atc ctt ttg agc tat 240
 His Leu Pro Leu Leu Lys Lys Gly Asp Pro Glu Ile Leu Leu Ser Tyr
 65 70 75 80
 gat ggg gat aag gca ggg cga aac gca gcc tat aaa gcg agc ttg atg 288
 Asp Gly Asp Lys Ala Gly Arg Asn Ala Ala Tyr Lys Ala Ser Leu Met
 85 90 95
 ttg gct aaa gag caa agg agg gga ggg gtg att ttg ttt gaa aac aac 336
 Leu Ala Lys Glu Gln Arg Arg Gly Gly Val Ile Leu Phe Glu Asn Asn
 100 105 110
 ctg gat cca gcg gat atg atc gct aat ggc cag att gaa acc tta aaa 384
 Leu Asp Pro Ala Asp Met Ile Ala Asn Gly Gln Ile Glu Thr Leu Lys
 115 120 125
 aat tgg cta tcg cac ccc atg gct ttt att gag ttt gtt tta agg cgc 432
 Asn Trp Leu Ser His Pro Met Ala Phe Ile Glu Phe Val Leu Arg Arg
 130 135 140
 atg gcg gat tcc tat ctt tta gac gat cct tta gaa aaa gat aag gct 480
 Met Ala Asp Ser Tyr Leu Leu Asp Asp Pro Leu Glu Lys Asp Lys Ala
 145 150 155 160
 ctt aaa gaa atg tta ggg ttt tta aaa aac ttt tcc ttg ctt tta caa 528
 Leu Lys Glu Met Leu Gly Phe Leu Lys Asn Phe Ser Leu Leu Leu Gln
 165 170 175

agc gaa tac aag ccc tta atc gct acc ctt ttg caa gcg cct ttg cat 576
 Ser Glu Tyr Lys Pro Leu Ile Ala Thr Leu Leu Gln Ala Pro Leu His
 180 185 190
 gtt tta ggg att aga gag cga gtc tct ttt cag cct ttt tac ccc aaa 624
 Val Leu Gly Ile Arg Glu Arg Val Ser Phe Gln Pro Phe Tyr Pro Lys
 195 200 205
 aca gaa aaa ccc aat cgc cct caa 648
 Thr Glu Lys Pro Asn Arg Pro Gln
 210 215
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 <211> 216
 <212> PRT
 <213> *Helicobacter pylori*
 <400> 222
 Lys Tyr Ile Asn Ser Pro Gln Ser Lys Leu Phe Asp Lys Ser Ser Leu
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 Leu Tyr Gly Tyr His Leu Ala Lys Glu His Ile Tyr Lys Gln Lys Gln
 20 25 30
 Val Ile Val Thr Glu Gly Tyr Leu Asp Val Ile Leu Leu His Gln Ala
 35 40 45
 Gly Phe Lys Asn Ala Ile Ala Thr Leu Gly Thr Ala Leu Thr Pro Ser
 50 55 60
 His Leu Pro Leu Leu Lys Lys Gly Asp Pro Glu Ile Leu Leu Ser Tyr
 65 70 75 80
 Asp Gly Asp Lys Ala Gly Arg Asn Ala Ala Tyr Lys Ala Ser Leu Met
 85 90 95
 Leu Ala Lys Glu Gln Arg Arg Gly Gly Val Ile Leu Phe Glu Asn Asn
 100 105 110
 Leu Asp Pro Ala Asp Met Ile Ala Asn Gly Gln Ile Glu Thr Leu Lys
 115 120 125
 Asn Trp Leu Ser His Pro Met Ala Phe Ile Glu Phe Val Leu Arg Arg
 130 135 140
 Met Ala Asp Ser Tyr Leu Leu Asp Asp Pro Leu Glu Lys Asp Lys Ala
 145 150 155 160
 Leu Lys Glu Met Leu Gly Phe Leu Lys Asn Phe Ser Leu Leu Leu Gln
 165 170 175
 Ser Glu Tyr Lys Pro Leu Ile Ala Thr Leu Leu Gln Ala Pro Leu His
 180 185 190
 Val Leu Gly Ile Arg Glu Arg Val Ser Phe Gln Pro Phe Tyr Pro Lys
 195 200 205
 Thr Glu Lys Pro Asn Arg Pro Gln
 210 215
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 <221> CDS
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 <400> 223
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 Thr Gln Met Ala Phe Asp Phe Asn Thr Pro Leu Leu Gln Val Gln His
 1 5 10 15
 cac cat gcc cac ttt tta gcg agc gtc tta gac gca ttg tta caa gat 96
 His His Ala His Phe Leu Ala Ser Val Leu Asp Ala Leu Leu Gln Asp
 20 25 30
 ccg cat tta aat cac ccc ttt ata ggc att gtc tgg gat ggg agt ggg 144
 Pro His Leu Asn His Pro Phe Ile Gly Ile Val Trp Asp Gly Ser Gly
 35 40 45
 gct tat gaa aat aag att tat ggg gcg gag tgt ttt gtg ggg gat ttg 192
 Ala Tyr Glu Asn Lys Ile Tyr Gly Ala Glu Cys Phe Val Gly Asp Leu

50 55 60
 gaa cgc att gaa gaa acc gcc agg ttt gaa gaa ttt tgg ctt tta ggg 240
 Glu Arg Ile Glu Glu Thr Ala Arg Phe Glu Glu Phe Trp Leu Leu Gly
 65 70 75 80
 ggg caa aaa gcg atc aaa gag cct aga cgc ctg gtt tta gaa atc gct 288
 Gly Gln Lys Ala Ile Lys Glu Pro Arg Arg Leu Val Leu Glu Ile Ala
 85 90 95
 tta aaa cac caa ctc aac aag ctt tta aag cgc gtt caa aag cat ttt 336
 Leu Lys His Gln Leu Asn Lys Leu Leu Lys Arg Val Gln Lys His Phe
 100 105 110
 aaa gaa gac gaa tta gaa att ttc caa caa atg cat gac aaa aaa att 384
 Lys Glu Asp Glu Leu Glu Ile Phe Gln Gln Met His Asp Lys Lys Ile
 115 120 125
 caa agc ata gcc acc aat tcc ata ggg cgt ttg ttt gat ata gta gcg 432
 Gln Ser Ile Ala Thr Asn Ser Ile Gly Arg Leu Phe Asp Ile Val Ala
 130 135 140
 ttt agt ttg gat tta aca gga acg att agc ttt gaa gca gag agc ggg 480
 Phe Ser Leu Asp Leu Thr Gly Thr Ile Ser Phe Glu Ala Glu Ser Gly
 145 150 155 160
 cag gtt tta gaa aat cta gcc tta caa agc gat gag atc gct ttt tac 528
 Gln Val Leu Glu Asn Leu Ala Leu Gln Ser Asp Glu Ile Ala Phe Tyr
 165 170 175
 cct ttt gaa atc aaa aac agc gtg gtg tgt ttg aaa gaa ttt tat caa 576
 Pro Phe Glu Ile Lys Asn Ser Val Val Cys Leu Lys Glu Phe Tyr Gln
 180 185 190
 gcg ttt gaa aag gat ttg ggc gtt tta gag cct gaa cgc atc gct aag 624
 Ala Phe Glu Lys Asp Leu Gly Val Leu Glu Pro Glu Arg Ile Ala Lys
 195 200 205
 aaa ttt ttt aac agc cta gta gaa atc att acc gct tta atc gtg cct 672
 Lys Phe Phe Asn Ser Leu Val Glu Ile Ile Thr Ala Leu Ile Val Pro
 210 215 220
 ttt aaa gag cat gtg gtg gtg tgc agt ggg ggc gtg ttt tgc aac caa 720
 Phe Lys Glu His Val Val Val Cys Ser Gly Gly Val Phe Cys Asn Gln
 225 230 235 240
 tta tta tgc gaa caa tta gcc aaa cga ttg aga ggg cta aag agg cag 768
 Leu Leu Cys Glu Gln Leu Ala Lys Arg Leu Arg Gly Leu Lys Arg Gln
 245 250 255
 tat ttt ttc cac aag cat ttc ccc cct aat gac agc agt atc cct atc 816
 Tyr Phe Phe His Lys His Phe Pro Pro Asn Asp Ser Ser Ile Pro Ile
 260 265 270
 ggt caa gcc tta atg gcg tat ttc aac cct aca atc atc aaa aaa gga 864
 Gly Gln Ala Leu Met Ala Tyr Phe Asn Pro Thr Ile Ile Lys Lys Gly
 275 280 285

<210> 224

<211> 288

<212> PRT

<213> Helicobacter pylori

<400> 224

Thr Gln Met Ala Phe Asp Phe Asn Thr Pro Leu Leu Gln Val Gln His
 1 5 10 15
 His His Ala His Phe Leu Ala Ser Val Leu Asp Ala Leu Leu Gln Asp
 20 25 30
 Pro His Leu Asn His Pro Phe Ile Gly Ile Val Trp Asp Gly Ser Gly
 35 40 45
 Ala Tyr Glu Asn Lys Ile Tyr Gly Ala Glu Cys Phe Val Gly Asp Leu
 50 55 60
 Glu Arg Ile Glu Glu Thr Ala Arg Phe Glu Glu Phe Trp Leu Leu Gly
 65 70 75 80
 Gly Gln Lys Ala Ile Lys Glu Pro Arg Arg Leu Val Leu Glu Ile Ala
 85 90 95
 Leu Lys His Gln Leu Asn Lys Leu Leu Lys Arg Val Gln Lys His Phe

100 105 110
 Lys Glu Asp Glu Leu Glu Ile Phe Gln Gln Met His Asp Lys Lys Ile
 115 120 125
 Gln Ser Ile Ala Thr Asn Ser Ile Gly Arg Leu Phe Asp Ile Val Ala
 130 135 140
 Phe Ser Leu Asp Leu Thr Gly Thr Ile Ser Phe Glu Ala Glu Ser Gly
 145 150 155 160
 Gln Val Leu Glu Asn Leu Ala Leu Gln Ser Asp Glu Ile Ala Phe Tyr
 165 170 175
 Pro Phe Glu Ile Lys Asn Ser Val Val Cys Leu Lys Glu Phe Tyr Gln
 180 185 190
 Ala Phe Glu Lys Asp Leu Gly Val Leu Glu Pro Glu Arg Ile Ala Lys
 195 200 205
 Lys Phe Phe Asn Ser Leu Val Glu Ile Ile Thr Ala Leu Ile Val Pro
 210 215 220
 Phe Lys Glu His Val Val Val Cys Ser Gly Gly Val Phe Cys Asn Gln
 225 230 235 240
 Leu Leu Cys Glu Gln Leu Ala Lys Arg Leu Arg Gly Leu Lys Arg Gln
 245 250 255
 Tyr Phe Phe His Lys His Phe Pro Pro Asn Asp Ser Ser Ile Pro Ile
 260 265 270
 Gly Gln Ala Leu Met Ala Tyr Phe Asn Pro Thr Ile Ile Lys Lys Gly
 275 280 285
 <210> 225
 <211> 159
 <212> DNA
 <213> Helicobacter pylori
 <220>
 <221> CDS
 <222> (1)..(159)
 <400> 225
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 Gln Gly Ile Leu Pro Pro Thr Ile Asn Gln Glu Met Pro Asp Pro Glu
 1 5 10 15
 tgc gat ttg gat tat atc cct aat gcg gcc aga gaa aag cga gtg gat 96
 Cys Asp Leu Asp Tyr Ile Pro Asn Ala Ala Arg Glu Lys Arg Val Asp
 20 25 30
 gca gtg atg agt aac tca ttt ggt ttt ggt ggc act aat ggt gtt gtg 144
 Ala Val Met Ser Asn Ser Phe Gly Phe Gly Gly Thr Asn Gly Val Val
 35 40 45
 att ttc aaa aaa gcc 159
 Ile Phe Lys Lys Ala
 50
 <210> 226
 <211> 53
 <212> PRT
 <213> Helicobacter pylori
 <400> 226
 Gln Gly Ile Leu Pro Pro Thr Ile Asn Gln Glu Met Pro Asp Pro Glu
 1 5 10 15
 Cys Asp Leu Asp Tyr Ile Pro Asn Ala Ala Arg Glu Lys Arg Val Asp
 20 25 30
 Ala Val Met Ser Asn Ser Phe Gly Phe Gly Gly Thr Asn Gly Val Val
 35 40 45
 Ile Phe Lys Lys Ala
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 <210> 227
 <211> 1293
 <212> DNA
 <213> Helicobacter pylori
 <220>

<221> CDS

<222> (1)..(1293)

<400> 227

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ttt ggg aat aag cag ttg caa ctt caa atc agt cag aaa gat tct gag 48
Phe Gly Asn Lys Gln Leu Gln Leu Gln Ile Ser Gln Lys Asp Ser Glu
1 5 10 15
att gcg gag tta aaa aaa gaa gtc aat ctt tat caa agc ctt tta aat 96
Ile Ala Glu Leu Lys Lys Glu Val Asn Leu Tyr Gln Ser Leu Leu Asn
20 25 30
ttg tgc ttg cat gag ggt ttt gta ggt att aaa aac aat aaa gtc gtt 144
Leu Cys Leu His Glu Gly Phe Val Gly Ile Lys Asn Asn Lys Val Val
35 40 45
ttt aaa agt ggg aat ctt gca agc ttg aac aat tta gaa gaa caa agc 192
Phe Lys Ser Gly Asn Leu Ala Ser Leu Asn Asn Leu Glu Glu Gln Ser
50 55 60
gtt cat ttt aaa gaa aat gca gag agc gtt aat tta caa ggg gtt tct 240
Val His Phe Lys Glu Asn Ala Glu Ser Val Asn Leu Gln Gly Val Ser
65 70 75 80
tat tct tta aaa agc caa aat att gat ggc gtg cag tat ttt tca ttg 288
Tyr Ser Leu Lys Ser Gln Asn Ile Asp Gly Val Gln Tyr Phe Ser Leu
85 90 95
gct aaa aac aca agt tgt gtg ggg gaa tac cat aaa aat gat ttg ttt 336
Ala Lys Asn Thr Ser Cys Val Gly Glu Tyr His Lys Asn Asp Leu Phe
100 105 110
aag act ttt tgc gcg agc tta aaa gaa ggc tta gag aac gcg caa gaa 384
Lys Thr Phe Cys Ala Ser Leu Lys Glu Gly Leu Glu Asn Ala Gln Glu
115 120 125
agc atg cag tat ttc cat caa gaa acc ggt gct ctt tta aat gca gct 432
Ser Met Gln Tyr Phe His Gln Glu Thr Gly Ala Leu Leu Asn Ala Ala
130 135 140
aaa aat ggc gaa gcg cat tct act gaa gga ttg ggg acg gtt aat aaa 480
Lys Asn Gly Glu Ala His Ser Thr Glu Gly Leu Gly Thr Val Asn Lys
145 150 155 160
acg ggg caa gac att gaa tcg ctt tat gaa aag atg caa aac gcc act 528
Thr Gly Gln Asp Ile Glu Ser Leu Tyr Glu Lys Met Gln Asn Ala Thr
165 170 175
tcg cta gcg gac tct ctc aac caa cgg agc aat gaa atc act caa gtc 576
Ser Leu Ala Asp Ser Leu Asn Gln Arg Ser Asn Glu Ile Thr Gln Val
180 185 190
att tct ttg att gat gat att gca gaa caa acc aat cta tta gcc cta 624
Ile Ser Leu Ile Asp Asp Ile Ala Glu Gln Thr Asn Leu Leu Ala Leu
195 200 205
aat gcc gct att gag gcc gcg cga gcg ggc gag cat ggg aga ggg ttt 672
Asn Ala Ala Ile Glu Ala Ala Arg Ala Gly Glu His Gly Arg Gly Phe
210 215 220
gcg gtg gtg gct gat gag gtg aga aaa ctc gct gaa aaa acc caa aaa 720
Ala Val Val Ala Asp Glu Val Arg Lys Leu Ala Glu Lys Thr Gln Lys
225 230 235 240
gcc act aaa gaa atc gct gtt gtc gtt aaa agc atg caa caa gaa gcg 768
Ala Thr Lys Glu Ile Ala Val Val Val Lys Ser Met Gln Gln Glu Ala
245 250 255
aac gat att caa acc aat acc cac gat att aat tct att gta agc tct 816
Asn Asp Ile Gln Thr Asn Thr His Asp Ile Asn Ser Ile Val Ser Ser
260 265 270
att aag ggc gat gtg gaa gag ctt aaa tcc acc gta aaa aat aac atg 864
Ile Lys Gly Asp Val Glu Glu Leu Lys Ser Thr Val Lys Asn Asn Met
275 280 285
att gtt gcg caa gcg gca aaa tac acc atc tac aat atc aat aac cgg 912
Ile Val Ala Gln Ala Ala Lys Tyr Thr Ile Tyr Asn Ile Asn Asn Arg
290 295 300
gtg ttt tgc ggt ttg gcc aaa ctt gat cat gtg gtc ttt aaa aac aat 960

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Val Phe Cys Gly Leu Ala Lys Leu Asp His Val Val Phe Lys Asn Asn
 305 310 315 320
 ctt tat ggc atg gtt ttt ggt ctc aat tcc ttt gat att acc agc cat 1008
 Leu Tyr Gly Met Val Phe Gly Leu Asn Ser Phe Asp Ile Thr Ser His
 325 330 335
 aag aat tgc cgt tta ggc aaa tgg tat tat gag ggc gcg ggc aaa gag 1056
 Lys Asn Cys Arg Leu Gly Lys Trp Tyr Tyr Glu Gly Ala Gly Lys Glu
 340 345 350
 aat ttt tcc aac act tca ggc tat aga gct tta gaa agc cac cat gca 1104
 Asn Phe Ser Asn Thr Ser Gly Tyr Arg Ala Leu Glu Ser His His Ala
 355 360 365
 agc gtg cat gct gaa gct aat gat ttg gtt aaa gcc gtt caa gaa gac 1152
 Ser Val His Ala Glu Ala Asn Asp Leu Val Lys Ala Val Gln Glu Asp
 370 375 380
 cac att acc gat tca aaa tac cta gag cat aaa gtg cat tta atg gaa 1200
 His Ile Thr Asp Ser Lys Tyr Leu Glu His Lys Val His Leu Met Glu
 385 390 395 400
 gat agt gct aaa cat gtt aga gaa aat att gat aag atg ttt tac gaa 1248
 Asp Ser Ala Lys His Val Arg Glu Asn Ile Asp Lys Met Phe Tyr Glu
 405 410 415
 aaa caa gat gaa ctc aat aaa atc att gaa aaa att caa aaa ggc 1293
 Lys Gln Asp Glu Leu Asn Lys Ile Ile Glu Lys Ile Gln Lys Gly
 420 425 430

<210> 228

<211> 431

<212> PRT

<213> *Helicobacter pylori*

<400> 228

Phe Gly Asn Lys Gln Leu Gln Leu Gln Ile Ser Gln Lys Asp Ser Glu
 1 5 10 15
 Ile Ala Glu Leu Lys Lys Glu Val Asn Leu Tyr Gln Ser Leu Leu Asn
 20 25 30
 Leu Cys Leu His Glu Gly Phe Val Gly Ile Lys Asn Asn Lys Val Val
 35 40 45
 Phe Lys Ser Gly Asn Leu Ala Ser Leu Asn Asn Leu Glu Glu Gln Ser
 50 55 60
 Val His Phe Lys Glu Asn Ala Glu Ser Val Asn Leu Gln Gly Val Ser
 65 70 75 80
 Tyr Ser Leu Lys Ser Gln Asn Ile Asp Gly Val Gln Tyr Phe Ser Leu
 85 90 95
 Ala Lys Asn Thr Ser Cys Val Gly Glu Tyr His Lys Asn Asp Leu Phe
 100 105 110
 Lys Thr Phe Cys Ala Ser Leu Lys Glu Gly Leu Glu Asn Ala Gln Glu
 115 120 125
 Ser Met Gln Tyr Phe His Gln Glu Thr Gly Ala Leu Leu Asn Ala Ala
 130 135 140
 Lys Asn Gly Glu Ala His Ser Thr Glu Gly Leu Gly Thr Val Asn Lys
 145 150 155 160
 Thr Gly Gln Asp Ile Glu Ser Leu Tyr Glu Lys Met Gln Asn Ala Thr
 165 170 175
 Ser Leu Ala Asp Ser Leu Asn Gln Arg Ser Asn Glu Ile Thr Gln Val
 180 185 190
 Ile Ser Leu Ile Asp Asp Ile Ala Glu Gln Thr Asn Leu Leu Ala Leu
 195 200 205
 Asn Ala Ala Ile Glu Ala Ala Arg Ala Gly Glu His Gly Arg Gly Phe
 210 215 220
 Ala Val Val Ala Asp Glu Val Arg Lys Leu Ala Glu Lys Thr Gln Lys
 225 230 235 240
 Ala Thr Lys Glu Ile Ala Val Val Val Lys Ser Met Gln Gln Glu Ala
 245 250 255
 Asn Asp Ile Gln Thr Asn Thr His Asp Ile Asn Ser Ile Val Ser Ser

260 265 270
 Ile Lys Gly Asp Val Glu Glu Leu Lys Ser Thr Val Lys Asn Asn Met
 275 280 285
 Ile Val Ala Gln Ala Ala Lys Tyr Thr Ile Tyr Asn Ile Asn Asn Arg
 290 295 300
 Val Phe Cys Gly Leu Ala Lys Leu Asp His Val Val Phe Lys Asn Asn
 305 310 315 320
 Leu Tyr Gly Met Val Phe Gly Leu Asn Ser Phe Asp Ile Thr Ser His
 325 330 335
 Lys Asn Cys Arg Leu Gly Lys Trp Tyr Tyr Glu Gly Ala Gly Lys Glu
 340 345 350
 Asn Phe Ser Asn Thr Ser Gly Tyr Arg Ala Leu Glu Ser His His Ala
 355 360 365
 Ser Val His Ala Glu Ala Asn Asp Leu Val Lys Ala Val Gln Glu Asp
 370 375 380
 His Ile Thr Asp Ser Lys Tyr Leu Glu His Lys Val His Leu Met Glu
 385 390 395 400
 Asp Ser Ala Lys His Val Arg Glu Asn Ile Asp Lys Met Phe Tyr Glu
 405 410 415
 Lys Gln Asp Glu Leu Asn Lys Ile Ile Glu Lys Ile Gln Lys Gly
 420 425 430

<210> 229

<211> 286

<212> DNA

<213> Helicobacter pylori

<220>

<221> CDS

<222> (1)..(285)

<400> 229

gat ttg aat gcg att tta gaa gat ctc aac agc aaa cag cta ttg cca 48
 Asp Leu Asn Ala Ile Leu Glu Asp Leu Asn Ser Lys Gln Leu Leu Pro
 1 5 10 15
 gaa tac gct tac aag gtt tat ggc gca gtg gtg agt caa aat aaa gac 96
 Glu Tyr Ala Tyr Lys Val Tyr Gly Ala Val Val Ser Gln Asn Lys Asp
 20 25 30
 ggc gtg tgg gtc ggc gat gaa gcc aaa acg aaa gcc aga aga aaa gaa 144
 Gly Val Trp Val Gly Asp Glu Ala Lys Thr Lys Ala Arg Arg Lys Glu
 35 40 45
 att ctt gaa aac aga aag gct aga tcc ata ccg gta aaa caa tgg atg 192
 Ile Leu Glu Asn Arg Lys Ala Arg Ser Ile Pro Val Lys Gln Trp Met
 50 55 60
 gag caa gaa aga aac gct atc ctt gaa aaa gag gct tcc aaa cag gtt 240
 Glu Gln Glu Arg Asn Ala Ile Leu Glu Lys Glu Ala Ser Lys Gln Val
 65 70 75 80
 aag cac atg tat gcg act agc ttt gat ctc tcg cct aag ttt ttg a 286
 Lys His Met Tyr Ala Thr Ser Phe Asp Leu Ser Pro Lys Phe Leu
 85 90 95

<210> 230

<211> 95

<212> PRT

<213> Helicobacter pylori

<400> 230

Asp Leu Asn Ala Ile Leu Glu Asp Leu Asn Ser Lys Gln Leu Leu Pro
 1 5 10 15
 Glu Tyr Ala Tyr Lys Val Tyr Gly Ala Val Val Ser Gln Asn Lys Asp
 20 25 30
 Gly Val Trp Val Gly Asp Glu Ala Lys Thr Lys Ala Arg Arg Lys Glu
 35 40 45
 Ile Leu Glu Asn Arg Lys Ala Arg Ser Ile Pro Val Lys Gln Trp Met
 50 55 60
 Glu Gln Glu Arg Asn Ala Ile Leu Glu Lys Glu Ala Ser Lys Gln Val

65	70	75	80
Lys His Met Tyr Ala Thr Ser Phe Asp Leu Ser Pro Lys Phe Leu			
85		90	95
<210> 231			
<211> 163			
<212> DNA			
<213> Helicobacter pylori			
<220>			
<221> CDS			
<222> (1)..(162)			
<400> 231			
aga cgc aat caa aaa agc gca tca aag ttt atc aac tat ccc tct aag			48
Arg Arg Asn Gln Lys Ser Ala Ser Lys Phe Ile Asn Tyr Pro Ser Lys			
1 5 10 15			
ttc ttc act cta tgc tat aat ctc tgt ttt aaa aca tta tgg aat gtt			96
Phe Phe Thr Leu Cys Tyr Asn Leu Cys Phe Lys Thr Leu Trp Asn Val			
20 25 30			
aga aga tat tca gca aaa ccc ttc caa acc aac caa tct aaa gaa aga			144
Arg Arg Tyr Ser Ala Lys Pro Phe Gln Thr Asn Gln Ser Lys Glu Arg			
35 40 45			
aac cat tca agg aac gca t			163
Asn His Ser Arg Asn Ala			
50			
<210> 232			
<211> 54			
<212> PRT			
<213> Helicobacter pylori			
<400> 232			
Arg Arg Asn Gln Lys Ser Ala Ser Lys Phe Ile Asn Tyr Pro Ser Lys			
1 5 10 15			
Phe Phe Thr Leu Cys Tyr Asn Leu Cys Phe Lys Thr Leu Trp Asn Val			
20 25 30			
Arg Arg Tyr Ser Ala Lys Pro Phe Gln Thr Asn Gln Ser Lys Glu Arg			
35 40 45			
Asn His Ser Arg Asn Ala			
50			
<210> 233			
<211> 222			
<212> DNA			
<213> Helicobacter pylori			
<220>			
<221> CDS			
<222> (1)..(222)			
<400> 233			
gac gat cgc tgc ttt ttt atc act gat tct cgc tac act caa gaa gct			48
Asp Asp Arg Ser Phe Phe Ile Thr Asp Ser Arg Tyr Thr Gln Glu Ala			
1 5 10 15			
aaa gaa agc gtt cag cct aaa aat ggc gtt tta gcg gaa gtg gta gaa			96
Lys Glu Ser Val Gln Pro Lys Asn Gly Val Leu Ala Glu Val Val Glu			
20 25 30			
tct agc gat tta gtg caa agc gcg att gat ttg att gtt aaa agt tgc			144
Ser Ser Asp Leu Val Gln Ser Ala Ile Asp Leu Ile Val Lys Ser Ser			
35 40 45			
gtt aaa aaa ctc ttt ttt gac ccc aat caa gtg aat tta caa acc tac			192
Val Lys Lys Leu Phe Phe Asp Pro Asn Gln Val Asn Leu Gln Thr Tyr			
50 55 60			
aag cgt tta aat tca gcg ctt ggg gat aag			222
Lys Arg Leu Asn Ser Ala Leu Gly Asp Lys			
65 70			
<210> 234			
<211> 74			

<212> PRT

<213> Helicobacter pylori

<400> 234

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Asp Asp Arg Ser Phe Phe Ile Thr Asp Ser Arg Tyr Thr Gln Glu Ala
 1          5          10          15
Lys Glu Ser Val Gln Pro Lys Asn Gly Val Leu Ala Glu Val Val Glu
          20          25          30
Ser Ser Asp Leu Val Gln Ser Ala Ile Asp Leu Ile Val Lys Ser Ser
          35          40          45
Val Lys Lys Leu Phe Phe Asp Pro Asn Gln Val Asn Leu Gln Thr Tyr
          50          55          60
Lys Arg Leu Asn Ser Ala Leu Gly Asp Lys
          65          70

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<210> 235

<211> 108

<212> DNA

<213> Helicobacter pylori

<220>

<221> CDS

<222> (1)..(108)

<400> 235

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ctt ggc tac aac atg gct tta atg gcg atg gtc aat att tta gcc gaa 48
Leu Gly Tyr Asn Met Ala Leu Met Ala Met Val Asn Ile Leu Ala Glu
 1          5          10          15
atg aaa gcg ttc caa gaa gcc caa aaa aac aac cct aat aac ccc att 96
Met Lys Ala Phe Gln Glu Ala Gln Lys Asn Asn Pro Asn Asn Pro Ile
          20          25          30
aac aat caa aaa
Asn Asn Gln Lys
          35

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<210> 236

<211> 36

<212> PRT

<213> Helicobacter pylori

<400> 236

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Leu Gly Tyr Asn Met Ala Leu Met Ala Met Val Asn Ile Leu Ala Glu
 1          5          10          15
Met Lys Ala Phe Gln Glu Ala Gln Lys Asn Asn Pro Asn Asn Pro Ile
          20          25          30
Asn Asn Gln Lys
          35

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<210> 237

<211> 381

<212> DNA

<213> Helicobacter pylori

<220>

<221> CDS

<222> (1)..(381)

<400> 237

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tct aaa gag agc ttg atg cat gcc att aat tca att aga gtg ggc atg 48
Ser Lys Glu Ser Leu Met His Ala Ile Asn Ser Ile Arg Val Gly Met
 1          5          10          15
cat ttt aaa gag ttg agt cag att tta gag agc act att aca gaa agg 96
His Phe Lys Glu Leu Ser Gln Ile Leu Glu Ser Thr Ile Thr Glu Arg
          20          25          30
ggc ttt gtg cct ttg aaa gga ttt tgc ggg cat ggc att ggt aaa aaa 144
Gly Phe Val Pro Leu Lys Gly Phe Cys Gly His Gly Ile Gly Lys Lys
          35          40          45
ccc cat gaa gag cca gag atc ccc aac tac cta gaa aaa ggc gtc aaa 192
Pro His Glu Glu Pro Glu Ile Pro Asn Tyr Leu Glu Lys Gly Val Lys
          50          55          60

```

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cct aat agc ggc cct aaa atc aaa gag ggc atg gta ttt tgc tta gag 240
Pro Asn Ser Gly Pro Lys Ile Lys Glu Gly Met Val Phe Cys Leu Glu
65 70 75 80
cct atg gtg tgt caa aaa cag ggc gag cct aaa ata cta gcg gat aag 288
Pro Met Val Cys Gln Lys Gln Gly Glu Pro Lys Ile Leu Ala Asp Lys
85 90 95
tgg agc gtg gtt tca gtg gat ggg ctt aac aca agc cac cat gag cat 336
Trp Ser Val Val Ser Val Asp Gly Leu Asn Thr Ser His His Glu His
100 105 110
act atc gcc ata gtt ggc aat aaa gca gtg att ctt acg gag cgt 381
Thr Ile Ala Ile Val Gly Asn Lys Ala Val Ile Leu Thr Glu Arg
115 120 125

```

<210> 238

<211> 127

<212> PRT

<213> Helicobacter pylori

<400> 238

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Ser Lys Glu Ser Leu Met His Ala Ile Asn Ser Ile Arg Val Gly Met
1 5 10 15
His Phe Lys Glu Leu Ser Gln Ile Leu Glu Ser Thr Ile Thr Glu Arg
20 25 30
Gly Phe Val Pro Leu Lys Gly Phe Cys Gly His Gly Ile Gly Lys Lys
35 40 45
Pro His Glu Glu Pro Glu Ile Pro Asn Tyr Leu Glu Lys Gly Val Lys
50 55 60
Pro Asn Ser Gly Pro Lys Ile Lys Glu Gly Met Val Phe Cys Leu Glu
65 70 75 80
Pro Met Val Cys Gln Lys Gln Gly Glu Pro Lys Ile Leu Ala Asp Lys
85 90 95
Trp Ser Val Val Ser Val Asp Gly Leu Asn Thr Ser His His Glu His
100 105 110
Thr Ile Ala Ile Val Gly Asn Lys Ala Val Ile Leu Thr Glu Arg
115 120 125

```

<210> 239

<211> 242

<212> DNA

<213> Helicobacter pylori

<220>

<221> CDS

<222> (1)..(240)

<400> 239

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cag ctc agc ggt ggg caa aaa caa cga gtg gcg atc gct agg agt tta 48
Gln Leu Ser Gly Gly Gln Lys Gln Arg Val Ala Ile Ala Arg Ser Leu
1 5 10 15
gcg aat tgc cct gat tta ttg ctt tgc gat gaa gcc aca tcc gcg cta 96
Ala Asn Cys Pro Asp Leu Leu Leu Cys Asp Glu Ala Thr Ser Ala Leu
20 25 30
gat tct aaa acc acg cat tct att tta acg ctt tta agc ggc att caa 144
Asp Ser Lys Thr Thr His Ser Ile Leu Thr Leu Leu Ser Gly Ile Gln
35 40 45
aaa aag ctt gat ttg agc atc gtt ttc atc acg cat gaa att gaa gtg 192
Lys Lys Leu Asp Leu Ser Ile Val Phe Ile Thr His Glu Ile Glu Val
50 55 60
gtt aaa gaa ttg tgc aat caa atg tgc gtg atc agc agc ggc gaa atc 240
Val Lys Glu Leu Cys Asn Gln Met Cys Val Ile Ser Ser Gly Glu Ile
65 70 75 80
gt 242

```

<210> 240

<211> 80

<212> PRT

<213> Helicobacter pylori

<400> 240

Gln Leu Ser Gly Gly Gln Lys Gln Arg Val Ala Ile Ala Arg Ser Leu
 1 5 10 15
 Ala Asn Cys Pro Asp Leu Leu Leu Cys Asp Glu Ala Thr Ser Ala Leu
 20 25 30
 Asp Ser Lys Thr Thr His Ser Ile Leu Thr Leu Leu Ser Gly Ile Gln
 35 40 45
 Lys Lys Leu Asp Leu Ser Ile Val Phe Ile Thr His Glu Ile Glu Val
 50 55 60
 Val Lys Glu Leu Cys Asn Gln Met Cys Val Ile Ser Ser Gly Glu Ile
 65 70 75 80

<210> 241

<211> 471

<212> DNA

<213> Helicobacter pylori

<220>

<221> CDS

<222> (1)..(471)

<400> 241

tat ggc aag caa agc ttg agt tct ttt gcc aat aat ttt gtg cct gga 48
 Tyr Gly Lys Gln Ser Leu Ser Ser Phe Ala Asn Asn Phe Val Pro Gly
 1 5 10 15
 ggc ttg aat caa gcc ctt gat aaa ata ggc tct agc tct gat gcc aaa 96
 Gly Leu Asn Gln Ala Leu Asp Lys Ile Gly Ser Ser Ser Asp Ala Lys
 20 25 30
 gac tta cag aac ttc ttg gat aaa acg act ttt ggg gat att tta aat 144
 Asp Leu Gln Asn Phe Leu Asp Lys Thr Thr Phe Gly Asp Ile Leu Asn
 35 40 45
 caa atg att gaa caa gcc ccc tta atc aat aaa ctc att tct tgg ctg 192
 Gln Met Ile Glu Gln Ala Pro Leu Ile Asn Lys Leu Ile Ser Trp Leu
 50 55 60
 ggt ccg cag gat ttg agc gtt tta gtg aat atc gct tta aat agc atc 240
 Gly Pro Gln Asp Leu Ser Val Leu Val Asn Ile Ala Leu Asn Ser Ile
 65 70 75 80
 act aac cct agt aaa gag ctg act agc acc att tct agc ata ggt gaa 288
 Thr Asn Pro Ser Lys Glu Leu Thr Ser Thr Ile Ser Ser Ile Gly Glu
 85 90 95
 aaa gcg tta aat gac tta tta ggc gat ggc gta gtg aat aaa atc atg 336
 Lys Ala Leu Asn Asp Leu Leu Gly Asp Gly Val Val Asn Lys Ile Met
 100 105 110
 agc aat caa gtc tta ggg caa atg atc aat aaa atc att gct gat aag 384
 Ser Asn Gln Val Leu Gly Gln Met Ile Asn Lys Ile Ile Ala Asp Lys
 115 120 125
 ggc ttt gga ggc gtt tat cag caa ggt tta ggc tcc ata ctg cct caa 432
 Gly Phe Gly Gly Val Tyr Gln Gln Gly Leu Gly Ser Ile Leu Pro Gln
 130 135 140
 tct tta caa gat gaa ttg aag aaa ttg ggc atg ggc tct 471
 Ser Leu Gln Asp Glu Leu Lys Lys Leu Gly Met Gly Ser
 145 150 155

<210> 242

<211> 157

<212> PRT

<213> Helicobacter pylori

<400> 242

Tyr Gly Lys Gln Ser Leu Ser Ser Phe Ala Asn Asn Phe Val Pro Gly
 1 5 10 15
 Gly Leu Asn Gln Ala Leu Asp Lys Ile Gly Ser Ser Ser Asp Ala Lys
 20 25 30
 Asp Leu Gln Asn Phe Leu Asp Lys Thr Thr Phe Gly Asp Ile Leu Asn
 35 40 45
 Gln Met Ile Glu Gln Ala Pro Leu Ile Asn Lys Leu Ile Ser Trp Leu

50 55 60
 Gly Pro Gln Asp Leu Ser Val Leu Val Asn Ile Ala Leu Asn Ser Ile
 65 70 75 80
 Thr Asn Pro Ser Lys Glu Leu Thr Ser Thr Ile Ser Ser Ile Gly Glu
 85 90 95
 Lys Ala Leu Asn Asp Leu Leu Gly Asp Gly Val Val Asn Lys Ile Met
 100 105 110
 Ser Asn Gln Val Leu Gly Gln Met Ile Asn Lys Ile Ile Ala Asp Lys
 115 120 125
 Gly Phe Gly Gly Val Tyr Gln Gln Gly Leu Gly Ser Ile Leu Pro Gln
 130 135 140
 Ser Leu Gln Asp Glu Leu Lys Lys Leu Gly Met Gly Ser
 145 150 155

<210> 243

<211> 278

<212> DNA

<213> Helicobacter pylori

<220>

<221> CDS

<222> (1)..(276)

<400> 243

ggg aat atc acc gtt gat ggg cct tta aga gtg aat aat caa gtg ggt 48
 Gly Asn Ile Thr Val Asp Gly Pro Leu Arg Val Asn Asn Gln Val Gly
 1 5 10 15
 ggt tat gct ttg gca gga tca agc gcg aat ttt gag ttt aag gct ggt 96
 Gly Tyr Ala Leu Ala Gly Ser Ser Ala Asn Phe Glu Phe Lys Ala Gly
 20 25 30
 acg gat acc aaa aac ggc aca gcc act ttt aat aac gat att agt ttg 144
 Thr Asp Thr Lys Asn Gly Thr Ala Thr Phe Asn Asn Asp Ile Ser Leu
 35 40 45
 gga aga ttt gtg aat tta aaa gtg gat gct cat aca gct aat ttt aaa 192
 Gly Arg Phe Val Asn Leu Lys Val Asp Ala His Thr Ala Asn Phe Lys
 50 55 60
 ggt att gat act ggt aat ggt ggt ttc aac acc tta gat ttt agt ggc 240
 Gly Ile Asp Thr Gly Asn Gly Gly Phe Asn Thr Leu Asp Phe Ser Gly
 65 70 75 80
 gtt aca ggt aag gtc aat atc aac aag ctc att acg gc 278
 Val Thr Gly Lys Val Asn Ile Asn Lys Leu Ile Thr
 85 90

<210> 244

<211> 92

<212> PRT

<213> Helicobacter pylori

<400> 244

Gly Asn Ile Thr Val Asp Gly Pro Leu Arg Val Asn Asn Gln Val Gly
 1 5 10 15
 Gly Tyr Ala Leu Ala Gly Ser Ser Ala Asn Phe Glu Phe Lys Ala Gly
 20 25 30
 Thr Asp Thr Lys Asn Gly Thr Ala Thr Phe Asn Asn Asp Ile Ser Leu
 35 40 45
 Gly Arg Phe Val Asn Leu Lys Val Asp Ala His Thr Ala Asn Phe Lys
 50 55 60
 Gly Ile Asp Thr Gly Asn Gly Gly Phe Asn Thr Leu Asp Phe Ser Gly
 65 70 75 80
 Val Thr Gly Lys Val Asn Ile Asn Lys Leu Ile Thr
 85 90

<210> 245

<211> 901

<212> DNA

<213> Helicobacter pylori

<220>

<221> CDS

<222> (1)..(900)

<400> 245

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aat ggc gcg agt ggt aca ggc agt ggg aat ggc acc agt caa atc aac 48
Asn Gly Ala Ser Gly Thr Gly Ser Gly Asn Gly Thr Ser Gln Ile Asn
1 5 10 15
aca gcc tac cag atg ctc aca gac gcc agc gat ggg aaa tta ggg act 96
Thr Ala Tyr Gln Met Leu Thr Asp Ala Ser Asp Gly Lys Leu Gly Thr
20 25 30
tat agt agt agt agt ggc agt aat aac ggc tat acg cca tgc aat agc 144
Tyr Ser Ser Ser Ser Gly Ser Asn Asn Gly Tyr Thr Pro Cys Asn Ser
35 40 45
acc aat ggg agc aat aaa acg agt ggg aac aat tgt tat gaa ccc aac 192
Thr Asn Gly Ser Asn Lys Thr Ser Gly Asn Asn Cys Tyr Glu Pro Asn
50 55 60
aaa caa caa aac gcc acc acc gca acc gcc aca acc gac agc aat tta 240
Lys Gln Gln Asn Ala Thr Thr Ala Thr Ala Thr Thr Asp Ser Asn Leu
65 70 75 80
caa aaa gtc tat aat gac gcc caa aaa ata gcc aac att atc gcc agc 288
Gln Lys Val Tyr Asn Asp Ala Gln Lys Ile Ala Asn Ile Ile Ala Ser
85 90 95
tct ggg aac aat aaa ggc gtt gaa aac ggc tta aaa caa ttc ttt gaa 336
Ser Gly Asn Asn Lys Gly Val Glu Asn Gly Leu Lys Gln Phe Phe Glu
100 105 110
gcg tta aaa aat aat agc agc agt ctc agt aat tta tgt ggt aat ggt 384
Ala Leu Lys Asn Asn Ser Ser Ser Leu Ser Asn Leu Cys Gly Asn Gly
115 120 125
agt agc ggt agt agt ggc act act tgc tcc ggt tgg ctt atc aac ctt 432
Ser Ser Gly Ser Ser Gly Thr Cys Ser Gly Trp Leu Ile Asn Leu
130 135 140
tta ggg gca atc ccc acc aat gga gtg agc gat acg aat aat tta att 480
Leu Gly Ala Ile Pro Thr Asn Gly Val Ser Asp Thr Asn Asn Leu Ile
145 150 155 160
aat ctg ctc act gaa ttc att aaa acc gcc ggg ttt atc caa aat aat 528
Asn Leu Leu Thr Glu Phe Ile Lys Thr Ala Gly Phe Ile Gln Asn Asn
165 170 175
gat agt agt gta tct act agt ctt aca agc gct ttt caa gcc att acg 576
Asp Ser Ser Val Ser Thr Ser Leu Thr Ser Ala Phe Gln Ala Ile Thr
180 185 190
agc gct att tct caa ggg ttt caa gcc tta caa aac gat att agc cct 624
Ser Ala Ile Ser Gln Gly Phe Gln Ala Leu Gln Asn Asp Ile Ser Pro
195 200 205
aat gcg att tta acc ttg ctc caa gag att act tct aac acc acc acc 672
Asn Ala Ile Leu Thr Leu Leu Gln Glu Ile Thr Ser Asn Thr Thr Thr
210 215 220
att cag tca ttc tcg caa acc tta cgg cag ctt tta ggg gat aaa aca 720
Ile Gln Ser Phe Ser Gln Thr Leu Arg Gln Leu Leu Gly Asp Lys Thr
225 230 235 240
ttc ttt atg gcg caa caa aag ctc att gat gcg atg att aac gcc aga 768
Phe Phe Met Ala Gln Gln Lys Leu Ile Asp Ala Met Ile Asn Ala Arg
245 250 255
aat cag gtt caa aac gcg caa aat caa gcc aat aac tac ggc tct caa 816
Asn Gln Val Gln Asn Ala Gln Asn Gln Ala Asn Asn Tyr Gly Ser Gln
260 265 270
ccc gtt tta agc cag tat gcg gcc gct aaa agc acc caa cat ggc atg 864
Pro Val Leu Ser Gln Tyr Ala Ala Ala Lys Ser Thr Gln His Gly Met
275 280 285
agc aat ggt tta ggg gtt ggt ttg ggc tat aaa tac t 901
Ser Asn Gly Leu Gly Val Gly Leu Gly Tyr Lys Tyr
290 295 300

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<210> 246

<211> 300

<212> PRT

<213> Helicobacter pylori

<400> 246

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Asn Gly Ala Ser Gly Thr Gly Ser Gly Asn Gly Thr Ser Gln Ile Asn
 1           5           10           15
Thr Ala Tyr Gln Met Leu Thr Asp Ala Ser Asp Gly Lys Leu Gly Thr
          20           25           30
Tyr Ser Ser Ser Ser Gly Ser Asn Asn Gly Tyr Thr Pro Cys Asn Ser
          35           40           45
Thr Asn Gly Ser Asn Lys Thr Ser Gly Asn Asn Cys Tyr Glu Pro Asn
          50           55           60
Lys Gln Gln Asn Ala Thr Thr Ala Thr Ala Thr Thr Asp Ser Asn Leu
          65           70           75           80
Gln Lys Val Tyr Asn Asp Ala Gln Lys Ile Ala Asn Ile Ile Ala Ser
          85           90           95
Ser Gly Asn Asn Lys Gly Val Glu Asn Gly Leu Lys Gln Phe Phe Glu
          100          105          110
Ala Leu Lys Asn Asn Ser Ser Ser Leu Ser Asn Leu Cys Gly Asn Gly
          115          120          125
Ser Ser Gly Ser Ser Gly Thr Thr Cys Ser Gly Trp Leu Ile Asn Leu
          130          135          140
Leu Gly Ala Ile Pro Thr Asn Gly Val Ser Asp Thr Asn Asn Leu Ile
          145          150          155          160
Asn Leu Leu Thr Glu Phe Ile Lys Thr Ala Gly Phe Ile Gln Asn Asn
          165          170          175
Asp Ser Ser Val Ser Thr Ser Leu Thr Ser Ala Phe Gln Ala Ile Thr
          180          185          190
Ser Ala Ile Ser Gln Gly Phe Gln Ala Leu Gln Asn Asp Ile Ser Pro
          195          200          205
Asn Ala Ile Leu Thr Leu Leu Gln Glu Ile Thr Ser Asn Thr Thr Thr
          210          215          220
Ile Gln Ser Phe Ser Gln Thr Leu Arg Gln Leu Leu Gly Asp Lys Thr
          225          230          235          240
Phe Phe Met Ala Gln Gln Lys Leu Ile Asp Ala Met Ile Asn Ala Arg
          245          250          255
Asn Gln Val Gln Asn Ala Gln Asn Gln Ala Asn Asn Tyr Gly Ser Gln
          260          265          270
Pro Val Leu Ser Gln Tyr Ala Ala Ala Lys Ser Thr Gln His Gly Met
          275          280          285
Ser Asn Gly Leu Gly Val Gly Leu Gly Tyr Lys Tyr
          290          295          300

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<210> 247

<211> 147

<212> DNA

<213> Helicobacter pylori

<220>

<221> CDS

<222> (1)..(147)

<400> 247

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caa tac gac ttt aag gcg atg ttt act ccc ttg atc atg caa gcg cag      48
Gln Tyr Asp Phe Lys Ala Met Phe Thr Pro Leu Ile Met Gln Ala Gln
 1           5           10           15
ttg agc tta aga aac att gat aat ttt gtg gaa aaa ggc tct gct ttg      96
Leu Ser Leu Arg Asn Ile Asp Asn Phe Val Glu Lys Gly Ser Ala Leu
          20           25           30
ata gat aaa ttt gac gct aac ccc tat aaa acg att ttt gga gaa agg      144
Ile Asp Lys Phe Asp Ala Asn Pro Tyr Lys Thr Ile Phe Gly Glu Arg
          35           40           45
aaa
Lys

```

147

<210> 248

<211> 49

<212> PRT

<213> Helicobacter pylori

<400> 248

Gln Tyr Asp Phe Lys Ala Met Phe Thr Pro Leu Ile Met Gln Ala Gln
 1 5 10 15
 Leu Ser Leu Arg Asn Ile Asp Asn Phe Val Glu Lys Gly Ser Ala Leu
 20 25 30
 Ile Asp Lys Phe Asp Ala Asn Pro Tyr Lys Thr Ile Phe Gly Glu Arg
 35 40 45

Lys

<210> 249

<211> 249

<212> DNA

<213> Helicobacter pylori

<220>

<221> CDS

<222> (1)..(249)

<400> 249

tcc aag ctg gat ttg aaa gac att tat gcg ttt tta aaa aat tta gac 48
 Ser Lys Leu Asp Leu Lys Asp Ile Tyr Ala Phe Leu Lys Asn Leu Asp
 1 5 10 15
 aaa gaa aat ttt gat tcc aga gaa aat cag agg gaa agg att gaa agc 96
 Lys Glu Asn Phe Asp Ser Arg Glu Asn Gln Arg Glu Arg Ile Glu Ser
 20 25 30
 ctg tta gag agc gtt aac agg cat aag atc ccc tta aac gag caa gaa 144
 Leu Leu Glu Ser Val Asn Arg His Lys Ile Pro Leu Asn Glu Gln Glu
 35 40 45
 ttg caa gcc ttt gat tta gcg atc aag gct aac agc tct tat tac aag 192
 Leu Gln Ala Phe Asp Leu Ala Ile Lys Ala Asn Ser Ser Tyr Tyr Lys
 50 55 60
 ctc agc tat aat ctt tta ccc ctg ctt tta agc ctt tta tcc aaa aag 240
 Leu Ser Tyr Asn Leu Leu Pro Leu Leu Leu Ser Leu Leu Ser Lys Lys
 65 70 75 80
 aaa acg cca 249
 Lys Thr Pro

<210> 250

<211> 83

<212> PRT

<213> Helicobacter pylori

<400> 250

Ser Lys Leu Asp Leu Lys Asp Ile Tyr Ala Phe Leu Lys Asn Leu Asp
 1 5 10 15
 Lys Glu Asn Phe Asp Ser Arg Glu Asn Gln Arg Glu Arg Ile Glu Ser
 20 25 30
 Leu Leu Glu Ser Val Asn Arg His Lys Ile Pro Leu Asn Glu Gln Glu
 35 40 45
 Leu Gln Ala Phe Asp Leu Ala Ile Lys Ala Asn Ser Ser Tyr Tyr Lys
 50 55 60
 Leu Ser Tyr Asn Leu Leu Pro Leu Leu Leu Ser Leu Leu Ser Lys Lys
 65 70 75 80

Lys Thr Pro

<210> 251

<211> 618

<212> DNA

<213> Helicobacter pylori

<220>

<221> CDS

<222> (1)..(618)

<400> 251

gag ttt aga agt ttt ata gac aag cat tat aac cac tct ttt gag ccg 48
 Glu Phe Arg Ser Phe Ile Asp Lys His Tyr Asn His Ser Phe Glu Pro
 1 5 10 15
 cta gag gtt tta ggc tat att tat gcg tta ttg tat tcc cca aac tac 96
 Leu Glu Val Leu Gly Tyr Ile Tyr Ala Leu Leu Tyr Ser Pro Asn Tyr
 20 25 30
 cgc aag cgt tat gaa gac ttc ctt aaa aac gat tac cct aaa atc ctt 144
 Arg Lys Arg Tyr Glu Asp Phe Leu Lys Asn Asp Tyr Pro Lys Ile Leu
 35 40 45
 ttc aca aac aat aaa gat ttg ttt agg gct tta agc ctt tta ggg att 192
 Phe Thr Asn Asn Lys Asp Leu Phe Arg Ala Leu Ser Leu Leu Gly Ile
 50 55 60
 gaa cta atc ggc ttg cat gtc tta aac caa gaa agc ctg aat tac agc 240
 Glu Leu Ile Gly Leu His Val Leu Asn Gln Glu Ser Leu Asn Tyr Ser
 65 70 75 80
 ttt gga aaa tta aaa gac gcc acc ata ggc gaa tcc tgc tat aaa gaa 288
 Phe Gly Lys Leu Lys Asp Ala Thr Ile Gly Glu Ser Cys Tyr Lys Glu
 85 90 95
 gag cat aac ccc atc atc aaa aaa ccc tct cat aac gag cca gac caa 336
 Glu His Asn Pro Ile Ile Lys Lys Pro Ser His Asn Glu Pro Asp Gln
 100 105 110
 cgg ctt tat atc aac cat agc gct tat ttt agg ggg gtg agt caa gaa 384
 Arg Leu Tyr Ile Asn His Ser Ala Tyr Phe Arg Gly Val Ser Gln Glu
 115 120 125
 att tat gat tat aga ata ggg ggg tat ggc gtt tta gac aaa tat tta 432
 Ile Tyr Asp Tyr Arg Ile Gly Gly Tyr Gly Val Leu Asp Lys Tyr Leu
 130 135 140
 aaa agc cat aaa aac gag cct tgc gac ttt gat cat gta act aat atc 480
 Lys Ser His Lys Asn Glu Pro Cys Asp Phe Asp His Val Thr Asn Ile
 145 150 155 160
 att aaa gtc atc gca cgc acg att gaa atc caa aaa acg ctt gga ttt 528
 Ile Lys Val Ile Ala Arg Thr Ile Glu Ile Gln Lys Thr Leu Gly Phe
 165 170 175
 tta acg agc gat ttg ccc cat tta aaa ggg aat gac agc aaa gcc tta 576
 Leu Thr Ser Asp Leu Pro His Leu Lys Gly Asn Asp Ser Lys Ala Leu
 180 185 190
 atg caa gaa atc ttg caa aat cca ccc ccc ccc ccc ccc att 618
 Met Gln Glu Ile Leu Gln Asn Pro Pro Pro Pro Pro Pro Ile
 195 200 205

<210> 252

<211> 206

<212> PRT

<213> *Helicobacter pylori*

<400> 252

Glu Phe Arg Ser Phe Ile Asp Lys His Tyr Asn His Ser Phe Glu Pro
 1 5 10 15
 Leu Glu Val Leu Gly Tyr Ile Tyr Ala Leu Leu Tyr Ser Pro Asn Tyr
 20 25 30
 Arg Lys Arg Tyr Glu Asp Phe Leu Lys Asn Asp Tyr Pro Lys Ile Leu
 35 40 45
 Phe Thr Asn Asn Lys Asp Leu Phe Arg Ala Leu Ser Leu Leu Gly Ile
 50 55 60
 Glu Leu Ile Gly Leu His Val Leu Asn Gln Glu Ser Leu Asn Tyr Ser
 65 70 75 80
 Phe Gly Lys Leu Lys Asp Ala Thr Ile Gly Glu Ser Cys Tyr Lys Glu
 85 90 95
 Glu His Asn Pro Ile Ile Lys Lys Pro Ser His Asn Glu Pro Asp Gln
 100 105 110
 Arg Leu Tyr Ile Asn His Ser Ala Tyr Phe Arg Gly Val Ser Gln Glu
 115 120 125
 Ile Tyr Asp Tyr Arg Ile Gly Gly Tyr Gly Val Leu Asp Lys Tyr Leu

130 135 140
 Lys Ser His Lys Asn Glu Pro Cys Asp Phe Asp His Val Thr Asn Ile
 145 150 155 160
 Ile Lys Val Ile Ala Arg Thr Ile Glu Ile Gln Lys Thr Leu Gly Phe
 165 170 175
 Leu Thr Ser Asp Leu Pro His Leu Lys Gly Asn Asp Ser Lys Ala Leu
 180 185 190
 Met Gln Glu Ile Leu Gln Asn Pro Pro Pro Pro Pro Pro Ile
 195 200 205
 <210> 253
 <211> 1269
 <212> DNA
 <213> *Helicobacter pylori*
 <220>
 <221> CDS
 <222> (1)..(1269)
 <400> 253
 ttt gac aga gaa aga atc cct gaa agg gtg gtg cat gct aaa gga agc 48
 Phe Asp Arg Glu Arg Ile Pro Glu Arg Val Val His Ala Lys Gly Ser
 1 5 10 15
 gga gct tat ggc act ttc act gtg act aaa gac atc act aaa tac act 96
 Gly Ala Tyr Thr Phe Thr Val Thr Lys Asp Ile Thr Lys Tyr Thr
 20 25 30
 aaa gcg aaa att ttc tct aaa gtg ggc aaa aaa acc gaa tgc ttc ttc 144
 Lys Ala Lys Ile Phe Ser Lys Val Gly Lys Lys Thr Glu Cys Phe Phe
 35 40 45
 aga ttt tct act gtg gct ggt gaa aga ggc agt gcg gat gcg gtg aga 192
 Arg Phe Ser Thr Val Ala Gly Glu Arg Gly Ser Ala Asp Ala Val Arg
 50 55 60
 gac cct aga ggt ttt gcg atg aag tat tac act gaa gaa ggt aac tgg 240
 Asp Pro Arg Gly Phe Ala Met Lys Tyr Tyr Thr Glu Glu Gly Asn Trp
 65 70 75 80
 gat tta gtg ggg aac aac acg cct gtt ttc ttt atc cgt gat gcg atc 288
 Asp Leu Val Gly Asn Asn Thr Pro Val Phe Phe Ile Arg Asp Ala Ile
 85 90 95
 aaa ttc cct gat ttc atc cac act caa aaa cga gat cct caa acc aat 336
 Lys Phe Pro Asp Phe Ile His Thr Gln Lys Arg Asp Pro Gln Thr Asn
 100 105 110
 ttg cct aac cat gac atg gta tgg gat ttt tgg agt aat gtt cct gaa 384
 Leu Pro Asn His Asp Met Val Trp Asp Phe Trp Ser Asn Val Pro Glu
 115 120 125
 agc tta tac caa gta aca tgg gtt atg agc gat agg ggt att cct aaa 432
 Ser Leu Tyr Gln Val Thr Trp Val Met Ser Asp Arg Gly Ile Pro Lys
 130 135 140
 tct ttc cgc cac atg gat ggt ttt ggc agc cac act ttc agt ctt atc 480
 Ser Phe Arg His Met Asp Gly Phe Gly Ser His Thr Phe Ser Leu Ile
 145 150 155 160
 aac gcg aaa ggc gaa cgc ttt tgg gtg aaa ttc cac ttc cac acc atg 528
 Asn Ala Lys Gly Glu Arg Phe Trp Val Lys Phe His Phe His Thr Met
 165 170 175
 caa ggc gtt aag cat ttg act aac gaa gaa gcc gca gaa gtt agg aag 576
 Gln Gly Val Lys His Leu Thr Asn Glu Glu Ala Ala Glu Val Arg Lys
 180 185 190
 tat gat ccg gat tcc aat caa agg gat tta ttc aat gcg atc gct aga 624
 Tyr Asp Pro Asp Ser Asn Gln Arg Asp Leu Phe Asn Ala Ile Ala Arg
 195 200 205
 ggg gat ttc cca aaa tgg aaa tta agc att caa gtg atg cca gaa gaa 672
 Gly Asp Phe Pro Lys Trp Lys Leu Ser Ile Gln Val Met Pro Glu Glu
 210 215 220
 gat gct aag aag tat cga ttc cat ccg ttt gat gta act aaa att tgg 720
 Asp Ala Lys Lys Tyr Arg Phe His Pro Phe Asp Val Thr Lys Ile Trp

145 150 155 160
 Asn Ala Lys Gly Glu Arg Phe Trp Val Lys Phe His Phe His Thr Met
 165 170 175
 Gln Gly Val Lys His Leu Thr Asn Glu Glu Ala Ala Glu Val Arg Lys
 180 185 190
 Tyr Asp Pro Asp Ser Asn Gln Arg Asp Leu Phe Asn Ala Ile Ala Arg
 195 200 205
 Gly Asp Phe Pro Lys Trp Lys Leu Ser Ile Gln Val Met Pro Glu Glu
 210 215 220
 Asp Ala Lys Lys Tyr Arg Phe His Pro Phe Asp Val Thr Lys Ile Trp
 225 230 235 240
 Tyr Leu Gln Asp Tyr Pro Leu Met Glu Val Gly Ile Val Glu Leu Asn
 245 250 255
 Lys Asn Pro Glu Asn Tyr Phe Ala Glu Val Glu Gln Ala Ala Phe Ser
 260 265 270
 Pro Ala Asn Val Val Pro Gly Ile Gly Tyr Ser Pro Asp Arg Met Leu
 275 280 285
 Gln Gly Arg Leu Phe Ser Tyr Gly Asp Thr His Arg Tyr Arg Leu Gly
 290 295 300
 Val Asn Tyr Pro Gln Ile Pro Val Asn Lys Pro Arg Cys Pro Phe His
 305 310 315 320
 Ser Ser Ser Arg Asp Gly Tyr Met Gln Asn Gly Tyr Tyr Gly Ser Leu
 325 330 335
 Gln Asn Tyr Thr Pro Ser Ser Leu Pro Gly Tyr Lys Glu Asp Lys Ser
 340 345 350
 Ala Arg Asp Pro Lys Phe Asn Leu Ala His Ile Glu Lys Glu Phe Glu
 355 360 365
 Val Trp Asn Trp Asp Tyr Arg Ala Asp Asp Ser Asp Tyr Tyr Thr Gln
 370 375 380
 Pro Gly Asp Tyr Tyr Arg Ser Leu Pro Ala Asp Glu Lys Glu Arg Leu
 385 390 395 400
 His Asp Thr Ile Gly Glu Ser Leu Ala His Val Thr His Lys Glu Ile
 405 410 415
 Val Asp Lys Gln Leu Glu His
 420
 <210> 255
 <211> 1005
 <212> DNA
 <213> *Helicobacter pylori*
 <220>
 <221> CDS
 <222> (1)..(1005)
 <400> 255
 agc att att tat ccc ctt tat atg ggt ggg gca aga ttc acg atg gtg 48
 Ser Ile Ile Tyr Pro Leu Tyr Met Gly Gly Ala Arg Phe Thr Met Val
 1 5 10 15
 cgc att gcg gat ttg atg caa aaa gat gct aat gaa gtg tat cgt ttg 96
 Arg Ile Ala Asp Leu Met Gln Lys Asp Ala Asn Glu Val Tyr Arg Leu
 20 25 30
 aaa aag ctt tcc act ttt caa gag ctt gtg agc gtg tat tac ggc atg 144
 Lys Lys Leu Ser Thr Phe Gln Glu Leu Val Ser Val Tyr Tyr Gly Met
 35 40 45
 gtg tta aac gca gaa gtg gct gaa act tta gaa gag gtg gaa aaa ggc 192
 Val Leu Asn Ala Glu Val Ala Glu Thr Leu Glu Glu Val Glu Lys Gly
 50 55 60
 cat tat aag cat ttc caa aac gct ttg aaa atg caa aaa gtg ggg caa 240
 His Tyr Lys His Phe Gln Asn Ala Leu Lys Met Gln Lys Val Gly Gln
 65 70 75 80
 atc gct agg gta gaa acc tta ggc gct caa gtg gct tat gat aag gcc 288
 Ile Ala Arg Val Glu Thr Leu Gly Ala Gln Val Ala Tyr Asp Lys Ala
 85 90 95

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cat atc gct agc gtt aag gct aaa gac gtg tta gaa gtt tcg cag ctc 336
His Ile Ala Ser Val Lys Ala Lys Asp Val Leu Glu Val Ser Gln Leu
      100      105      110
tcg ttc aat tcc att tta tct agc aag gac gat tta gtg cct tca agc 384
Ser Phe Asn Ser Ile Leu Ser Ser Lys Asp Asp Leu Val Pro Ser Ser
      115      120      125
aaa tta gag atc cgc acg gag aaa aat ctg ccc gat ctg agc ttt ttt 432
Lys Leu Glu Ile Arg Thr Glu Lys Asn Leu Pro Asp Leu Ser Phe Phe
      130      135      140
gtt tct tcc acg ctc aat tcc tac ccg gtt tta aag act tta gaa aat 480
Val Ser Ser Thr Leu Asn Ser Tyr Pro Val Leu Lys Thr Leu Glu Asn
      145      150      155      160
cag att caa atc tct aaa gaa aac acg aaa tta cag atc gct aaa ttc 528
Gln Ile Gln Ile Ser Lys Glu Asn Thr Lys Leu Gln Ile Ala Lys Phe
      165      170      175
ttg ccc caa gtg agt ttt ttt ggc tct tat att atg aag caa aac aat 576
Leu Pro Gln Val Ser Phe Phe Gly Ser Tyr Ile Met Lys Gln Asn Asn
      180      185      190
tcg gtg ttt gaa gac atg atc cct agt tgg ttt gtg ggc gtg gcc ggg 624
Ser Val Phe Glu Asp Met Ile Pro Ser Trp Phe Val Gly Val Ala Gly
      195      200      205
cgc atg cct att ctt tct ccc aca ggc cgc att caa aaa tac caa gcg 672
Arg Met Pro Ile Leu Ser Pro Thr Gly Arg Ile Gln Lys Tyr Gln Ala
      210      215      220
agc aaa tta gcg gag ttg caa gtg agt agc gaa caa atc cag gct aaa 720
Ser Lys Leu Ala Glu Leu Gln Val Ser Ser Glu Gln Ile Gln Ala Lys
      225      230      235      240
aaa aac atg gaa tta tta gtg aat aag act tat aaa gag acg ctt tct 768
Lys Asn Met Glu Leu Val Asn Lys Thr Tyr Lys Glu Thr Leu Ser
      245      250      255
tat ttg aaa gaa tac aaa agc ttg ctt tct agc gtg gaa tta gcc aag 816
Tyr Leu Lys Glu Tyr Lys Ser Leu Leu Ser Ser Val Glu Leu Ala Lys
      260      265      270
gaa aac tta aaa ctc caa gag cag gct ttt tta caa ggc tta agc acg 864
Glu Asn Leu Lys Leu Gln Glu Gln Ala Phe Leu Gln Gly Leu Ser Thr
      275      280      285
aac gct caa gtc att gat gcg agg aac acg ctt tct tct atc gtc gtg 912
Asn Ala Gln Val Ile Asp Ala Arg Asn Thr Leu Ser Ser Ile Val Val
      290      295      300
gag caa aaa agc gtg gct tat aaa tac atc gtt tca tta gcg aat tta 960
Glu Gln Lys Ser Val Ala Tyr Lys Tyr Ile Val Ser Leu Ala Asn Leu
      305      310      315      320
atg gcg tta agc gat cat att gat tta ttt tat gaa ttt gtt tat 1005
Met Ala Leu Ser Asp His Ile Asp Leu Phe Tyr Glu Phe Val Tyr
      325      330      335

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<210> 256

<211> 335

<212> PRT

<213> *Helicobacter pylori*

<400> 256

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Ser Ile Ile Tyr Pro Leu Tyr Met Gly Gly Ala Arg Phe Thr Met Val
 1           5           10           15
Arg Ile Ala Asp Leu Met Gln Lys Asp Ala Asn Glu Val Tyr Arg Leu
      20      25      30
Lys Lys Leu Ser Thr Phe Gln Glu Leu Val Ser Val Tyr Tyr Gly Met
      35      40      45
Val Leu Asn Ala Glu Val Ala Glu Thr Leu Glu Glu Val Glu Lys Gly
      50      55      60
His Tyr Lys His Phe Gln Asn Ala Leu Lys Met Gln Lys Val Gly Gln
      65      70      75      80
Ile Ala Arg Val Glu Thr Leu Gly Ala Gln Val Ala Tyr Asp Lys Ala

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85 90 95
 His Ile Ala Ser Val Lys Ala Lys Asp Val Leu Glu Val Ser Gln Leu
 100 105 110
 Ser Phe Asn Ser Ile Leu Ser Ser Lys Asp Asp Leu Val Pro Ser Ser
 115 120 125
 Lys Leu Glu Ile Arg Thr Glu Lys Asn Leu Pro Asp Leu Ser Phe Phe
 130 135 140
 Val Ser Ser Thr Leu Asn Ser Tyr Pro Val Leu Lys Thr Leu Glu Asn
 145 150 155 160
 Gln Ile Gln Ile Ser Lys Glu Asn Thr Lys Leu Gln Ile Ala Lys Phe
 165 170 175
 Leu Pro Gln Val Ser Phe Phe Gly Ser Tyr Ile Met Lys Gln Asn Asn
 180 185 190
 Ser Val Phe Glu Asp Met Ile Pro Ser Trp Phe Val Gly Val Ala Gly
 195 200 205
 Arg Met Pro Ile Leu Ser Pro Thr Gly Arg Ile Gln Lys Tyr Gln Ala
 210 215 220
 Ser Lys Leu Ala Glu Leu Gln Val Ser Ser Glu Gln Ile Gln Ala Lys
 225 230 235 240
 Lys Asn Met Glu Leu Val Asn Lys Thr Tyr Lys Glu Thr Leu Ser
 245 250 255
 Tyr Leu Lys Glu Tyr Lys Ser Leu Leu Ser Ser Val Glu Leu Ala Lys
 260 265 270
 Glu Asn Leu Lys Leu Gln Glu Gln Ala Phe Leu Gln Gly Leu Ser Thr
 275 280 285
 Asn Ala Gln Val Ile Asp Ala Arg Asn Thr Leu Ser Ser Ile Val Val
 290 295 300
 Glu Gln Lys Ser Val Ala Tyr Lys Tyr Ile Val Ser Leu Ala Asn Leu
 305 310 315 320
 Met Ala Leu Ser Asp His Ile Asp Leu Phe Tyr Glu Phe Val Tyr
 325 330 335

<210> 257

<211> 296

<212> DNA

<213> *Helicobacter pylori*

<220>

<221> CDS

<222> (1)..(294)

<400> 257

gaa atc att aga gat att gct gat caa acc aat ctt tta gcc tta aac 48
 Glu Ile Ile Arg Asp Ile Ala Asp Gln Thr Asn Leu Leu Ala Leu Asn
 1 5 10 15
 gcc gct att gaa gcc gca agg gcc ggc gag cat ggc aga ggc ttt gcg 96
 Ala Ala Ile Glu Ala Ala Arg Ala Gly Glu His Gly Arg Gly Phe Ala
 20 25 30
 gtg gtg gct gat gag gta aga aag ctc gct gaa agg acg caa aaa tcg 144
 Val Val Ala Asp Glu Val Arg Lys Leu Ala Glu Arg Thr Gln Lys Ser
 35 40 45
 ctc agc gag att gaa gcc aat atc aat att tta gtg caa agc att tca 192
 Leu Ser Glu Ile Glu Ala Asn Ile Asn Ile Leu Val Gln Ser Ile Ser
 50 55 60
 gac acg agc gaa agc att aaa aac cag gtt aaa gaa gtg gaa gaa atc 240
 Asp Thr Ser Glu Ser Ile Lys Asn Gln Val Lys Glu Val Glu Glu Ile
 65 70 75 80
 aac gct tct att gaa gcc tta aga tcg gtt act gag ggc aat cta aaa 288
 Asn Ala Ser Ile Glu Ala Leu Arg Ser Val Thr Glu Gly Asn Leu Lys
 85 90 95
 atc gct ag 296
 Ile Ala
 <210> 258
 <211> 98

<212> PRT

<213> Helicobacter pylori

<400> 258

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Glu Ile Ile Arg Asp Ile Ala Asp Gln Thr Asn Leu Leu Ala Leu Asn
 1           5           10           15
Ala Ala Ile Glu Ala Ala Arg Ala Gly Glu His Gly Arg Gly Phe Ala
      20           25           30
Val Val Ala Asp Glu Val Arg Lys Leu Ala Glu Arg Thr Gln Lys Ser
      35           40           45
Leu Ser Glu Ile Glu Ala Asn Ile Asn Ile Leu Val Gln Ser Ile Ser
      50           55           60
Asp Thr Ser Glu Ser Ile Lys Asn Gln Val Lys Glu Val Glu Glu Ile
      65           70           75           80
Asn Ala Ser Ile Glu Ala Leu Arg Ser Val Thr Glu Gly Asn Leu Lys
      85           90           95

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Ile Ala

<210> 259

<211> 430

<212> DNA

<213> Helicobacter pylori

<220>

<221> CDS

<222> (1)..(429)

<400> 259

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att caa gct tta ctc gtg ggc gtt caa gaa gaa tat tac gct atc ccg      48
Ile Gln Ala Leu Leu Val Gly Val Gln Glu Glu Tyr Tyr Ala Ile Pro
 1           5           10           15
ctt tct tca gtg tta gaa acc gtg cgc atc agc cag gat gaa att tac      96
Leu Ser Ser Val Leu Glu Thr Val Arg Ile Ser Gln Asp Glu Ile Tyr
      20           25           30
acc gtt gat ggc aag agc gtg ttg cgt ttg aga gat gag gtg ctt tct      144
Thr Val Asp Gly Lys Ser Val Leu Arg Leu Arg Asp Glu Val Leu Ser
      35           40           45
ttg gtg cgc ctt tct gat att ttt aaa gta gat gct att ttg gaa tcc      192
Leu Val Arg Leu Ser Asp Ile Phe Lys Val Asp Ala Ile Leu Glu Ser
      50           55           60
aac tca gat gtg tat gtg gtt atc att ggc ttg gct gat caa aaa att      240
Asn Ser Asp Val Tyr Val Val Ile Ile Gly Leu Ala Asp Gln Lys Ile
      65           70           75           80
ggc gtg atc gtg gat tat tta atc ggt caa gaa gaa gtg gtc att aaa      288
Gly Val Ile Val Asp Tyr Leu Ile Gly Gln Glu Glu Val Val Ile Lys
      85           90           95
tct tta ggt tac tat ctt aaa aac act aga ggc att gct ggt gct acg      336
Ser Leu Gly Tyr Tyr Leu Lys Asn Thr Arg Gly Ile Ala Gly Ala Thr
      100           105           110
gtg aga ggc gat ggg aaa atc acc ctt att gta gat gtg ggg gcg atg      384
Val Arg Gly Asp Gly Lys Ile Thr Leu Ile Val Asp Val Gly Ala Met
      115           120           125
atg gat atg gca aaa agc atc aag gtc aat atc act acc tta atg a      430
Met Asp Met Ala Lys Ser Ile Lys Val Asn Ile Thr Thr Leu Met
      130           135           140

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<210> 260

<211> 143

<212> PRT

<213> Helicobacter pylori

<400> 260

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Ile Gln Ala Leu Leu Val Gly Val Gln Glu Glu Tyr Tyr Ala Ile Pro
 1           5           10           15
Leu Ser Ser Val Leu Glu Thr Val Arg Ile Ser Gln Asp Glu Ile Tyr
      20           25           30
Thr Val Asp Gly Lys Ser Val Leu Arg Leu Arg Asp Glu Val Leu Ser

```


35 40 45
 Leu Val Arg Leu Ser Asp Ile Phe Lys Val Asp Ala Ile Leu Glu Ser
 50 55 60
 Asn Ser Asp Val Tyr Val Val Ile Ile Gly Leu Ala Asp Gln Lys Ile
 65 70 75 80
 Gly Val Ile Val Asp Tyr Leu Ile Gly Gln Glu Glu Val Val Ile Lys
 85 90 95
 Ser Leu Gly Tyr Tyr Leu Lys Asn Thr Arg Gly Ile Ala Gly Ala Thr
 100 105 110
 Val Arg Gly Asp Gly Lys Ile Thr Leu Ile Val Asp Val Gly Ala Met
 115 120 125
 Met Asp Met Ala Lys Ser Ile Lys Val Asn Ile Thr Thr Leu Met
 130 135 140
 <210> 261
 <211> 497
 <212> DNA
 <213> *Helicobacter pylori*
 <220>
 <221> CDS
 <222> (1)..(495)
 <400> 261
 aaa att gga gtt tgt ggt cct gta gga agc ggt aaa acc gcc ttg att 48
 Lys Ile Gly Val Cys Gly Pro Val Gly Ser Gly Lys Thr Ala Leu Ile
 1 5 10 15
 gaa gct tta acg cgc cac atg tca aaa gat tat gac atg gcg gtc atc 96
 Glu Ala Leu Thr Arg His Met Ser Lys Asp Tyr Asp Met Ala Val Ile
 20 25 30
 act aat gat att tac acg aaa gaa gac gca gag ttt atg tgt aaa aat 144
 Thr Asn Asp Ile Tyr Thr Lys Glu Asp Ala Glu Phe Met Cys Lys Asn
 35 40 45
 tcg gtg atg cca cga gag agg atc att ggc gta gaa aca gga ggc tgt 192
 Ser Val Met Pro Arg Glu Arg Ile Ile Gly Val Glu Thr Gly Gly Cys
 50 55 60
 ccg cac acg gct att aga gaa gac gct tct atg aat tta gaa gcc gta 240
 Pro His Thr Ala Ile Arg Glu Asp Ala Ser Met Asn Leu Glu Ala Val
 65 70 75 80
 gaa gaa atg cat ggc cgt ttc cct aat ttg gaa ttg ctt ttg att gaa 288
 Glu Glu Met His Gly Arg Phe Pro Asn Leu Glu Leu Leu Leu Ile Glu
 85 90 95
 agc gga ggc gat aac ctt tca gcg aca ttc aac cca gag cta gcg gac 336
 Ser Gly Gly Asp Asn Leu Ser Ala Thr Phe Asn Pro Glu Leu Ala Asp
 100 105 110
 ttt acg atc ttt gtg att gat gtg gct gag ggc gat aaa atc ccc cga 384
 Phe Thr Ile Phe Val Ile Asp Val Ala Glu Gly Asp Lys Ile Pro Arg
 115 120 125
 aaa ggc ggg cca gga atc acg cgc tca gac ttg ctt gtc atc aat aag 432
 Lys Gly Gly Pro Gly Ile Thr Arg Ser Asp Leu Leu Val Ile Asn Lys
 130 135 140
 att gat tta gcc ccc tat gtg gga gcg gac ttg aaa gtc atg gaa agg 480
 Ile Asp Leu Ala Pro Tyr Val Gly Ala Asp Leu Lys Val Met Glu Arg
 145 150 155 160
 gat tct aaa aaa atg cg 497
 Asp Ser Lys Lys Met
 165
 <210> 262
 <211> 165
 <212> PRT
 <213> *Helicobacter pylori*
 <400> 262
 Lys Ile Gly Val Cys Gly Pro Val Gly Ser Gly Lys Thr Ala Leu Ile
 1 5 10 15

Glu Ala Leu Thr Arg His Met Ser Lys Asp Tyr Asp Met Ala Val Ile
 20 25 30
 Thr Asn Asp Ile Tyr Thr Lys Glu Asp Ala Glu Phe Met Cys Lys Asn
 35 40 45
 Ser Val Met Pro Arg Glu Arg Ile Ile Gly Val Glu Thr Gly Gly Cys
 50 55 60
 Pro His Thr Ala Ile Arg Glu Asp Ala Ser Met Asn Leu Glu Ala Val
 65 70 75 80
 Glu Glu Met His Gly Arg Phe Pro Asn Leu Glu Leu Leu Ile Glu
 85 90 95
 Ser Gly Gly Asp Asn Leu Ser Ala Thr Phe Asn Pro Glu Leu Ala Asp
 100 105 110
 Phe Thr Ile Phe Val Ile Asp Val Ala Glu Gly Asp Lys Ile Pro Arg
 115 120 125
 Lys Gly Gly Pro Gly Ile Thr Arg Ser Asp Leu Leu Val Ile Asn Lys
 130 135 140
 Ile Asp Leu Ala Pro Tyr Val Gly Ala Asp Leu Lys Val Met Glu Arg
 145 150 155 160
 Asp Ser Lys Lys Met
 165

<210> 263

<211> 402

<212> DNA

<213> *Helicobacter pylori*

<220>

<221> CDS

<222> (1)..(402)

<400> 263

ttt aaa acc agg caa ggc aaa gac ata gcc ata cgc ctt aaa gac gct 48
 Phe Lys Thr Arg Gln Gly Lys Asp Ile Ala Ile Arg Leu Lys Asp Ala
 1 5 10 15
 ccc aag ttg ggg ctc tct caa ggg gat att tta ttt aaa gaa gag aag 96
 Pro Lys Leu Gly Leu Ser Gln Gly Asp Ile Leu Phe Lys Glu Glu Lys
 20 25 30
 gaa att atc gcc gtt aat atc ttg gat tct gaa gtc att cac atc caa 144
 Glu Ile Ile Ala Val Asn Ile Leu Asp Ser Glu Val Ile His Ile Gln
 35 40 45
 gcc aag agc gtg gca gaa gta gcg aaa ata tgc tat gaa ata gga aac 192
 Ala Lys Ser Val Ala Glu Val Ala Lys Ile Cys Tyr Glu Ile Gly Asn
 50 55 60
 cgc cat gcg gct tta tac tat ggc gag tct caa ttt gaa ttt aaa aca 240
 Arg His Ala Ala Leu Tyr Tyr Gly Glu Ser Gln Phe Glu Phe Lys Thr
 65 70 75 80
 cca ttt gaa aag ccc acg cta gcg tta tta gaa aag cta ggg gtt caa 288
 Pro Phe Glu Lys Pro Thr Leu Ala Leu Leu Glu Lys Leu Gly Val Gln
 85 90 95
 aat cgt gtt tta agt tca aaa ttg gat tcc aaa gaa cgc tta acc gtg 336
 Asn Arg Val Leu Ser Ser Lys Leu Asp Ser Lys Glu Arg Leu Thr Val
 100 105 110
 agc atg ccc cat agt gag cct aat ttt aag gtc tca cta gcg agc gat 384
 Ser Met Pro His Ser Glu Pro Asn Phe Lys Val Ser Leu Ala Ser Asp
 115 120 125
 ttt aaa gtg gtc gta aaa 402
 Phe Lys Val Val Val Lys
 130

<210> 264

<211> 134

<212> PRT

<213> *Helicobacter pylori*

<400> 264

Phe Lys Thr Arg Gln Gly Lys Asp Ile Ala Ile Arg Leu Lys Asp Ala

1 5 10 15
 Pro Lys Leu Gly Leu Ser Gln Gly Asp Ile Leu Phe Lys Glu Glu Lys
 20 25 30
 Glu Ile Ile Ala Val Asn Ile Leu Asp Ser Glu Val Ile His Ile Gln
 35 40 45
 Ala Lys Ser Val Ala Glu Val Ala Lys Ile Cys Tyr Glu Ile Gly Asn
 50 55 60
 Arg His Ala Ala Leu Tyr Tyr Gly Glu Ser Gln Phe Glu Phe Lys Thr
 65 70 75 80
 Pro Phe Glu Lys Pro Thr Leu Ala Leu Leu Glu Lys Leu Gly Val Gln
 85 90 95
 Asn Arg Val Leu Ser Ser Lys Leu Asp Ser Lys Glu Arg Leu Thr Val
 100 105 110
 Ser Met Pro His Ser Glu Pro Asn Phe Lys Val Ser Leu Ala Ser Asp
 115 120 125
 Phe Lys Val Val Val Lys
 130

<210> 265

<211> 606

<212> DNA

<213> *Helicobacter pylori*

<220>

<221> CDS

<222> (1)..(606)

<400> 265

att aaa aga gcg gca aag gaa ttg aaa gag ggc atg tat gtg aat tta 48
 Ile Lys Arg Ala Ala Lys Glu Leu Lys Glu Gly Met Tyr Val Asn Leu
 1 5 10 15
 ggg ata ggc ttg ccc acg ctt gtg gct aat gaa gtg agc ggg atg aat 96
 Gly Ile Gly Leu Pro Thr Leu Val Ala Asn Glu Val Ser Gly Met Asn
 20 25 30
 atc gtt ttc caa agc gag aac ggg ctg tta ggg att ggc gct tac cct 144
 Ile Val Phe Gln Ser Glu Asn Gly Leu Leu Gly Ile Gly Ala Tyr Pro
 35 40 45
 tta gag ggg agc gtt gat gcg gat ctt atc aac gca gga aag gaa acc 192
 Leu Glu Gly Ser Val Asp Ala Asp Leu Ile Asn Ala Gly Lys Glu Thr
 50 55 60
 ata acc gtg gtg ccg ggc gct tcg ttt ttc aat agc gcg gat tcg ttt 240
 Ile Thr Val Val Pro Gly Ala Ser Phe Phe Asn Ser Ala Asp Ser Phe
 65 70 75 80
 gcg atg att cgt ggg ggg cat att gat tta gcg att tta ggg ggg atg 288
 Ala Met Ile Arg Gly Gly His Ile Asp Leu Ala Ile Leu Gly Gly Met
 85 90 95
 gaa gtc tca caa aat ggg gat ttg gct aat tgg atg atc cct aaa aag 336
 Glu Val Ser Gln Asn Gly Asp Leu Ala Asn Trp Met Ile Pro Lys Lys
 100 105 110
 ctc ata aag ggc atg gga ggg gct atg gat ttg gtg cat ggc gct aaa 384
 Leu Ile Lys Gly Met Gly Gly Ala Met Asp Leu Val His Gly Ala Lys
 115 120 125
 aaa gtg att gtg atc atg gag cat tgc aac aaa tac ggg gag tct aaa 432
 Lys Val Ile Val Ile Met Glu His Cys Asn Lys Tyr Gly Glu Ser Lys
 130 135 140
 gtg aaa aag gaa tgc tca ttg ccc tta aca gga aaa ggc gtg gtg cat 480
 Val Lys Lys Glu Cys Ser Leu Pro Leu Thr Gly Lys Gly Val Val His
 145 150 155 160
 caa ttg ata acg gat tta gcg gtg ttt gag ttt tcc aat aac gcc atg 528
 Gln Leu Ile Thr Asp Leu Ala Val Phe Glu Phe Ser Asn Asn Ala Met
 165 170 175
 aaa tta gtg gaa ttg caa gag ggg gtc agc ctt gat caa gtg aaa gaa 576
 Lys Leu Val Glu Leu Gln Glu Gly Val Ser Leu Asp Gln Val Lys Glu
 180 185 190

aag aca gaa gct gaa ttt gag gtg cgc tta
 Lys Thr Glu Ala Glu Phe Glu Val Arg Leu
 195 200

606

<210> 266

<211> 202

<212> PRT

<213> Helicobacter pylori

<400> 266

Ile Lys Arg Ala Ala Lys Glu Leu Lys Glu Gly Met Tyr Val Asn Leu
 1 5 10 15
 Gly Ile Gly Leu Pro Thr Leu Val Ala Asn Glu Val Ser Gly Met Asn
 20 25 30
 Ile Val Phe Gln Ser Glu Asn Gly Leu Leu Gly Ile Gly Ala Tyr Pro
 35 40 45
 Leu Glu Gly Ser Val Asp Ala Asp Leu Ile Asn Ala Gly Lys Glu Thr
 50 55 60
 Ile Thr Val Val Pro Gly Ala Ser Phe Phe Asn Ser Ala Asp Ser Phe
 65 70 75 80
 Ala Met Ile Arg Gly Gly His Ile Asp Leu Ala Ile Leu Gly Gly Met
 85 90 95
 Glu Val Ser Gln Asn Gly Asp Leu Ala Asn Trp Met Ile Pro Lys Lys
 100 105 110
 Leu Ile Lys Gly Met Gly Gly Ala Met Asp Leu Val His Gly Ala Lys
 115 120 125
 Lys Val Ile Val Ile Met Glu His Cys Asn Lys Tyr Gly Glu Ser Lys
 130 135 140
 Val Lys Lys Glu Cys Ser Leu Pro Leu Thr Gly Lys Gly Val Val His
 145 150 155 160
 Gln Leu Ile Thr Asp Leu Ala Val Phe Glu Phe Ser Asn Asn Ala Met
 165 170 175
 Lys Leu Val Glu Leu Gln Glu Gly Val Ser Leu Asp Gln Val Lys Glu
 180 185 190
 Lys Thr Glu Ala Glu Phe Glu Val Arg Leu
 195 200

<210> 267

<211> 336

<212> DNA

<213> Helicobacter pylori

<220>

<221> CDS

<222> (1)..(336)

<400> 267

ggg att gaa caa gac gct gat att gtt tta ttt tta tat aga ggc tat 48
 Gly Ile Glu Gln Asp Ala Asp Ile Val Leu Phe Leu Tyr Arg Gly Tyr
 1 5 10 15
 atc tat caa atg agg gct gaa gac aac aaa ata gac aaa ctc aaa aaa 96
 Ile Tyr Gln Met Arg Ala Glu Asp Asn Lys Ile Asp Lys Leu Lys Lys
 20 25 30
 gaa ggt aaa att gaa gag gcg caa gag ttg tac tta aaa gtt aat gaa 144
 Glu Gly Lys Ile Glu Glu Ala Gln Glu Leu Tyr Leu Lys Val Asn Glu
 35 40 45
 gaa agg cgt atc cac aag caa aat ggc agc att gaa gag gct gaa atc 192
 Glu Arg Arg Ile His Lys Gln Asn Gly Ser Ile Glu Glu Ala Glu Ile
 50 55 60
 att gtg gct aaa aac agg aat ggg gct aca gga acg gtt tat acg cgc 240
 Ile Val Ala Lys Asn Arg Asn Gly Ala Thr Gly Thr Val Tyr Thr Arg
 65 70 75 80
 ttt aac gct cct ttc acg cgc tat gaa gac atg ccc ata gat tcc cat 288
 Phe Asn Ala Pro Phe Thr Arg Tyr Glu Asp Met Pro Ile Asp Ser His
 85 90 95
 tta gaa gaa ggg caa gaa act aaa gtg gat tat gat ata gtt aca act 336

Leu Glu Glu Gly Gln Glu Thr Lys Val Asp Tyr Asp Ile Val Thr Thr
 100 105 110

<210> 268

<211> 112

<212> PRT

<213> Helicobacter pylori

<400> 268

Gly Ile Glu Gln Asp Ala Asp Ile Val Leu Phe Leu Tyr Arg Gly Tyr
 1 5 10 15
 Ile Tyr Gln Met Arg Ala Glu Asp Asn Lys Ile Asp Lys Leu Lys Lys
 20 25 30
 Glu Gly Lys Ile Glu Glu Ala Gln Glu Leu Tyr Leu Lys Val Asn Glu
 35 40 45
 Glu Arg Arg Ile His Lys Gln Asn Gly Ser Ile Glu Glu Ala Glu Ile
 50 55 60
 Ile Val Ala Lys Asn Arg Asn Gly Ala Thr Gly Thr Val Tyr Thr Arg
 65 70 75 80
 Phe Asn Ala Pro Phe Thr Arg Tyr Glu Asp Met Pro Ile Asp Ser His
 85 90 95
 Leu Glu Glu Gly Gln Glu Thr Lys Val Asp Tyr Asp Ile Val Thr Thr
 100 105 110

<210> 269

<211> 240

<212> DNA

<213> Helicobacter pylori

<220>

<221> CDS

<222> (1)..(240)

<400> 269

aat gcg att gag caa gat gaa atc act aaa aaa att gaa gca gaa gag 48
 Asn Ala Ile Glu Gln Asp Glu Ile Thr Lys Lys Ile Glu Ala Glu Glu
 1 5 10 15
 ttg tta gag cat gtc caa aaa gcg ctg aat caa atg agc gaa aga gag 96
 Leu Leu Glu His Val Gln Lys Ala Leu Asn Gln Met Ser Glu Arg Glu
 20 25 30
 caa atc ctt atc cag ctt tat tac ttt gaa gag ttg aat ttg agc gag 144
 Gln Ile Leu Ile Gln Leu Tyr Tyr Phe Glu Glu Leu Asn Leu Ser Glu
 35 40 45
 att aaa gag att tta ggc att act gaa tcg cgc att tct caa atc att 192
 Ile Lys Glu Ile Leu Gly Ile Thr Glu Ser Arg Ile Ser Gln Ile Ile
 50 55 60
 aaa gaa gtg att aaa aag gtg cgt aaa tcc tta gga gtg gat cat ggc 240
 Lys Glu Val Ile Lys Lys Val Arg Lys Ser Leu Gly Val Asp His Gly
 65 70 75 80

<210> 270

<211> 80

<212> PRT

<213> Helicobacter pylori

<400> 270

Asn Ala Ile Glu Gln Asp Glu Ile Thr Lys Lys Ile Glu Ala Glu Glu
 1 5 10 15
 Leu Leu Glu His Val Gln Lys Ala Leu Asn Gln Met Ser Glu Arg Glu
 20 25 30
 Gln Ile Leu Ile Gln Leu Tyr Tyr Phe Glu Glu Leu Asn Leu Ser Glu
 35 40 45
 Ile Lys Glu Ile Leu Gly Ile Thr Glu Ser Arg Ile Ser Gln Ile Ile
 50 55 60
 Lys Glu Val Ile Lys Lys Val Arg Lys Ser Leu Gly Val Asp His Gly
 65 70 75 80

<210> 271

<211> 219

<212> DNA

<213> Helicobacter pylori

<220>

<221> CDS

<222> (1)..(219)

<400> 271

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ggt gat gaa aaa aag ggt cat ttg att tta ggg gag gtg gag cag gat 48
Val Asp Glu Lys Lys Gly His Leu Ile Leu Gly Glu Val Glu Gln Asp
  1          5          10          15
aat ggc gtg ttt gaa agc agt ggg ggg agg gtg atc ttt gcc att ggt 96
Asn Gly Val Phe Glu Ser Ser Gly Gly Arg Val Ile Phe Ala Ile Gly
          20          25          30
agg gga aaa tcc tta tta gaa gcc aga aac cat gct tat gaa atc gct 144
Arg Gly Lys Ser Leu Leu Glu Ala Arg Asn His Ala Tyr Glu Ile Ala
          35          40          45
caa aag gtg cat ttt gaa ggc atg ttt tat cgc aag gat att ggt ttt 192
Gln Lys Val His Phe Glu Gly Met Phe Tyr Arg Lys Asp Ile Gly Phe
          50          55          60
aag gtg tta gat ttg aaa gaa tat tct 219
Lys Val Leu Asp Leu Lys Glu Tyr Ser
          65          70

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<210> 272

<211> 73

<212> PRT

<213> Helicobacter pylori

<400> 272

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Val Asp Glu Lys Lys Gly His Leu Ile Leu Gly Glu Val Glu Gln Asp
  1          5          10          15
Asn Gly Val Phe Glu Ser Ser Gly Gly Arg Val Ile Phe Ala Ile Gly
          20          25          30
Arg Gly Lys Ser Leu Leu Glu Ala Arg Asn His Ala Tyr Glu Ile Ala
          35          40          45
Gln Lys Val His Phe Glu Gly Met Phe Tyr Arg Lys Asp Ile Gly Phe
          50          55          60
Lys Val Leu Asp Leu Lys Glu Tyr Ser
          65          70

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<210> 273

<211> 672

<212> DNA

<213> Helicobacter pylori

<220>

<221> CDS

<222> (1)..(672)

<400> 273

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aaa gac gat tta gcg gaa atc atg ctt tta gcg gta agc cct ggc atg 48
Lys Asp Asp Leu Ala Glu Ile Met Leu Leu Ala Val Ser Pro Gly Met
  1          5          10          15
atg agg ggc gat gcg caa gat gtg caa tta aac atc ggt cca aat tgc 96
Met Arg Gly Asp Ala Gln Asp Val Gln Leu Asn Ile Gly Pro Asn Cys
          20          25          30
aag tta agg atc act tcg caa tcc ttt gaa aaa atc cat aac act gaa 144
Lys Leu Arg Ile Thr Ser Gln Ser Phe Glu Lys Ile His Asn Thr Glu
          35          40          45
gat ggg ttt gcc agc aga gac atg cat att gtt gtg ggg gaa aac gct 192
Asp Gly Phe Ala Ser Arg Asp Met His Ile Val Val Gly Glu Asn Ala
          50          55          60
ttt tta gat ttt gcg cct ttc ccg tta atc ccc ttt gaa aac gcg cat 240
Phe Leu Asp Phe Ala Pro Phe Pro Leu Ile Pro Phe Glu Asn Ala His
          65          70          75          80
ttt aag ggc aac acc acg att tct ttg cgc tct agc tct caa ttg ctc 288
Phe Lys Gly Asn Thr Thr Ile Ser Leu Arg Ser Ser Ser Gln Leu Leu

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	85	90	95	
tat agt gaa atc att gtc gca ggg cga gtg gcg cgc aat gag ttg ttt				336
Tyr Ser Glu Ile Ile Val Ala Gly Arg Val Ala Arg Asn Glu Leu Phe				
	100	105	110	
aaa ttc aac cgc ttg cac acc aaa atc tct att tta caa gat gag aaa				384
Lys Phe Asn Arg Leu His Thr Lys Ile Ser Ile Leu Gln Asp Glu Lys				
	115	120	125	
ccc atc tat tat gac aac acg att tta gat ccc aaa acc acc gac tta				432
Pro Ile Tyr Tyr Asp Asn Thr Ile Leu Asp Pro Lys Thr Thr Asp Leu				
	130	135	140	
aat aac atg tgc atg ttt gat ggc tat acg cat tat ttg aat ttg gtg				480
Asn Asn Met Cys Met Phe Asp Gly Tyr Thr His Tyr Leu Asn Leu Val				
	145	150	155	
ctt gtc aat tgc ccc ata gag ctc tct ggt gtg cga gaa tgc att gaa				528
Leu Val Asn Cys Pro Ile Glu Leu Ser Gly Val Arg Glu Cys Ile Glu				
	165	170	175	
gaa agc gaa ggg gtg gat ggg gca gtg agt gaa acc gct agt tct cat				576
Glu Ser Glu Gly Val Asp Gly Ala Val Ser Glu Thr Ala Ser Ser His				
	180	185	190	
tta tgc gtg aaa gct tta gcg aaa ggc tca gaa ccc tta ttg cat tta				624
Leu Cys Val Lys Ala Leu Ala Lys Gly Ser Glu Pro Leu Leu His Leu				
	195	200	205	
aga gaa aaa atc gct cgc ttg gtt acg caa acc acc acg caa aag gtt				672
Arg Glu Lys Ile Ala Arg Leu Val Thr Gln Thr Thr Thr Gln Lys Val				
	210	215	220	
<210> 274				
<211> 224				
<212> PRT				
<213> Helicobacter pylori				
<400> 274				
Lys Asp Asp Leu Ala Glu Ile Met Leu Leu Ala Val Ser Pro Gly Met				
	1	5	10	15
Met Arg Gly Asp Ala Gln Asp Val Gln Leu Asn Ile Gly Pro Asn Cys				
	20	25	30	
Lys Leu Arg Ile Thr Ser Gln Ser Phe Glu Lys Ile His Asn Thr Glu				
	35	40	45	
Asp Gly Phe Ala Ser Arg Asp Met His Ile Val Val Gly Glu Asn Ala				
	50	55	60	
Phe Leu Asp Phe Ala Pro Phe Pro Leu Ile Pro Phe Glu Asn Ala His				
	65	70	75	80
Phe Lys Gly Asn Thr Ile Ser Leu Arg Ser Ser Ser Gln Leu Leu				
	85	90	95	
Tyr Ser Glu Ile Ile Val Ala Gly Arg Val Ala Arg Asn Glu Leu Phe				
	100	105	110	
Lys Phe Asn Arg Leu His Thr Lys Ile Ser Ile Leu Gln Asp Glu Lys				
	115	120	125	
Pro Ile Tyr Tyr Asp Asn Thr Ile Leu Asp Pro Lys Thr Thr Asp Leu				
	130	135	140	
Asn Asn Met Cys Met Phe Asp Gly Tyr Thr His Tyr Leu Asn Leu Val				
	145	150	155	160
Leu Val Asn Cys Pro Ile Glu Leu Ser Gly Val Arg Glu Cys Ile Glu				
	165	170	175	
Glu Ser Glu Gly Val Asp Gly Ala Val Ser Glu Thr Ala Ser Ser His				
	180	185	190	
Leu Cys Val Lys Ala Leu Ala Lys Gly Ser Glu Pro Leu Leu His Leu				
	195	200	205	
Arg Glu Lys Ile Ala Arg Leu Val Thr Gln Thr Thr Thr Gln Lys Val				
	210	215	220	
<210> 275				
<211> 477				
<212> DNA				

<213> *Helicobacter pylori*

<220>

<221> CDS

<222> (1)..(477)

<400> 275

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acc cac att ata gtg cgc gat ttg caa ggc aat gaa cgc gtg tta agc 96
Thr His Ile Ile Val Arg Asp Leu Gln Gly Asn Glu Arg Val Leu Ser
          20          25          30
aat gaa gag att caa aag ctc atc aaa gaa gaa gaa gct aaa att gat 144
Asn Glu Glu Ile Gln Lys Leu Ile Lys Glu Glu Glu Ala Lys Ile Asp
          35          40          45
aac ggc acg agc aag ctt gtc cag cct aat aat gga ggg agt aat gaa 192
Asn Gly Thr Ser Lys Leu Val Gln Pro Asn Asn Gly Gly Ser Asn Glu
          50          55          60
ggc tca ggc ttt ggc ttg ggg agc gcg att tta ggg agc gcg gcg ggg 240
Gly Ser Gly Phe Gly Leu Gly Ser Ala Ile Leu Gly Ser Ala Ala Gly
65          70          75          80
gcg att tta ggg agt tat att ggt aat aag ctt ttc aat aac cct aat 288
Ala Ile Leu Gly Ser Tyr Ile Gly Asn Lys Leu Phe Asn Asn Pro Asn
          85          90          95
tac cag caa aac gcc caa cgg acc tac aaa tcc cca caa gct tac caa 336
Tyr Gln Gln Asn Ala Gln Arg Thr Tyr Lys Ser Pro Gln Ala Tyr Gln
          100          105          110
cgc tct caa aat tcc ttt tct aaa agt gcg ccc agt gct tca agc atg 384
Arg Ser Gln Asn Ser Phe Ser Lys Ser Ala Pro Ser Ala Ser Ser Met
          115          120          125
ggc gga gcg agt aag gga cag agc ggg ttt ttt ggc tct agt agg cct 432
Gly Gly Ala Ser Lys Gly Gln Ser Gly Phe Phe Gly Ser Ser Arg Pro
          130          135          140
act agt tca ccg gcg gta agc tct ggg aca agg ggc ttt aac tca 477
Thr Ser Ser Pro Ala Val Ser Ser Gly Thr Arg Gly Phe Asn Ser
145          150          155

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<210> 276

<211> 159

<212> PRT

<213> *Helicobacter pylori*

<400> 276

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Thr His Ile Ile Val Arg Asp Leu Gln Gly Asn Glu Arg Val Leu Ser
          20          25          30
Asn Glu Glu Ile Gln Lys Leu Ile Lys Glu Glu Glu Ala Lys Ile Asp
          35          40          45
Asn Gly Thr Ser Lys Leu Val Gln Pro Asn Asn Gly Gly Ser Asn Glu
          50          55          60
Gly Ser Gly Phe Gly Leu Gly Ser Ala Ile Leu Gly Ser Ala Ala Gly
65          70          75          80
Ala Ile Leu Gly Ser Tyr Ile Gly Asn Lys Leu Phe Asn Asn Pro Asn
          85          90          95
Tyr Gln Gln Asn Ala Gln Arg Thr Tyr Lys Ser Pro Gln Ala Tyr Gln
          100          105          110
Arg Ser Gln Asn Ser Phe Ser Lys Ser Ala Pro Ser Ala Ser Ser Met
          115          120          125
Gly Gly Ala Ser Lys Gly Gln Ser Gly Phe Phe Gly Ser Ser Arg Pro
          130          135          140
Thr Ser Ser Pro Ala Val Ser Ser Gly Thr Arg Gly Phe Asn Ser
145          150          155

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<210> 277

<211> 685

<212> DNA

<213> Helicobacter pylori

<220>

<221> CDS

<222> (1)..(684)

<400> 277

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1 5 10 15
ggg gtg gag att gta ggg ttg gag cat ttg gat aaa gtg att tat tta 96
Gly Val Glu Ile Val Gly Leu Glu His Leu Asp Lys Val Ile Tyr Leu
20 25 30
gat caa gcc ccc ata ggc aaa acc cca cga agc aac cct gcc act tac 144
Asp Gln Ala Pro Ile Gly Lys Thr Pro Arg Ser Asn Pro Ala Thr Tyr
35 40 45
acg gga gtg atg gat gaa atc agg att tta ttt gcc gag caa aaa gaa 192
Thr Gly Val Met Asp Glu Ile Arg Ile Leu Phe Ala Glu Gln Lys Glu
50 55 60
gct aaa att tta ggc tat agt gcg agc cgt ttt agc ttt aat gtt aaa 240
Ala Lys Ile Leu Gly Tyr Ser Ala Ser Arg Phe Ser Phe Asn Val Lys
65 70 75 80
gga ggg cgg tgc gag aaa tgc caa ggc gat ggg gac att aaa ata gaa 288
Gly Gly Arg Cys Glu Lys Cys Gln Gly Asp Gly Asp Ile Lys Ile Glu
85 90 95
atg cac ttt ttg cct gat gtg tta gtc caa tgc gat agc tgt aag ggc 336
Met His Phe Leu Pro Asp Val Leu Val Gln Cys Asp Ser Cys Lys Gly
100 105 110
gct aaa tac aac ccc caa act tta gaa atc aag gtg aaa ggc aaa tcc 384
Ala Lys Tyr Asn Pro Gln Thr Leu Glu Ile Lys Val Lys Gly Lys Ser
115 120 125
att gcc gat gtg ttg aac atg agc gtg gaa gag gct tat gaa ttt ttt 432
Ile Ala Asp Val Leu Asn Met Ser Val Glu Glu Ala Tyr Glu Phe Phe
130 135 140
gct aaa ttc cct aaa atc gcc gtg aag tta aaa acg ctt atg gat gtg 480
Ala Lys Phe Pro Lys Ile Ala Val Lys Leu Lys Thr Leu Met Asp Val
145 150 155 160
ggc tta ggc tat atc act tta ggg caa aac gct acg act tta agt ggg 528
Gly Leu Gly Tyr Ile Thr Leu Gly Gln Asn Ala Thr Thr Leu Ser Gly
165 170 175
ggg gag gct caa agg atc aaa tta gct aaa gaa ttg agt aaa aaa gac 576
Gly Glu Ala Gln Arg Ile Lys Leu Ala Lys Glu Leu Ser Lys Lys Asp
180 185 190
aca ggc aaa acc ctt tat att tta gat gag cct act acc ggt ttg cat 624
Thr Gly Lys Thr Leu Tyr Ile Leu Asp Glu Pro Thr Thr Gly Leu His
195 200 205
ttt gaa gac gtg aat cat ctt tta caa gtc ttg cat tct tta gtg gcg 672
Phe Glu Asp Val Asn His Leu Leu Gln Val Leu His Ser Leu Val Ala
210 215 220
tta ggc aat tct a 685
Leu Gly Asn Ser
225

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<210> 278

<211> 228

<212> PRT

<213> Helicobacter pylori

<400> 278

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Thr Ala Gln Thr Leu Leu Asn His Ala Lys Lys Thr Gln Ser Leu Asn
1 5 10 15
Gly Val Glu Ile Val Gly Leu Glu His Leu Asp Lys Val Ile Tyr Leu
20 25 30

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Asp Gln Ala Pro Ile Gly Lys Thr Pro Arg Ser Asn Pro Ala Thr Tyr
 35 40 45
 Thr Gly Val Met Asp Glu Ile Arg Ile Leu Phe Ala Glu Gln Lys Glu
 50 55 60
 Ala Lys Ile Leu Gly Tyr Ser Ala Ser Arg Phe Ser Phe Asn Val Lys
 65 70 75 80
 Gly Gly Arg Cys Glu Lys Cys Gln Gly Asp Gly Asp Ile Lys Ile Glu
 85 90 95
 Met His Phe Leu Pro Asp Val Leu Val Gln Cys Asp Ser Cys Lys Gly
 100 105 110
 Ala Lys Tyr Asn Pro Gln Thr Leu Glu Ile Lys Val Lys Gly Lys Ser
 115 120 125
 Ile Ala Asp Val Leu Asn Met Ser Val Glu Glu Ala Tyr Glu Phe Phe
 130 135 140
 Ala Lys Phe Pro Lys Ile Ala Val Lys Leu Lys Thr Leu Met Asp Val
 145 150 155 160
 Gly Leu Gly Tyr Ile Thr Leu Gly Gln Asn Ala Thr Thr Leu Ser Gly
 165 170 175
 Gly Glu Ala Gln Arg Ile Lys Leu Ala Lys Glu Leu Ser Lys Lys Asp
 180 185 190
 Thr Gly Lys Thr Leu Tyr Ile Leu Asp Glu Pro Thr Thr Gly Leu His
 195 200 205
 Phe Glu Asp Val Asn His Leu Leu Gln Val Leu His Ser Leu Val Ala
 210 215 220
 Leu Gly Asn Ser
 225

INTERNATIONAL SEARCH REPORT

International Application No
PCT/IB 00/00603

A. CLASSIFICATION OF SUBJECT MATTER

IPC 7	C12N15/10	C12Q1/68	C07K14/205	C12N15/31	C12N1/19
	C12N1/21	G06F17/00	C12N15/86	C07K16/12	A61K48/00
	A61K39/106	A61K39/40			

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)
IPC 7 C12N C12Q C07K G06F A61K

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practical, search terms used)

EPO-Internal, WPI Data, MEDLINE, CHEM ABS Data, BIOSIS, EMBL

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
Y	JAMES R. HUDSON ET AL.: "The complete set of predicted genes from <i>Saccharomyces cerevisiae</i> in a readily usable form" GENOME RESEARCH, vol. 7, no. 12, December 1997 (1997-12), pages 1169-1173, XP002127444 the whole document --- -/-	1-43

☒ Further documents are listed in the continuation of box C.☒ Patent family members are listed in annex.

* Special categories of cited documents:

- "A" document defining the general state of the art which is not considered to be of particular relevance
- "E" earlier document but published on or after the international filing date
- "L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)
- "O" document referring to an oral disclosure, use, exhibition or other means
- "P" document published prior to the international filing date but later than the priority date claimed

"T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention

"X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone

"Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art.

"Δ" document member of the same patent family

Date of the actual completion of the international search

27 September 2000

Date of mailing of the international search report

11. 10. 00

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Montero Lopez, B

INTERNATIONAL SEARCH REPORT

International Application No

PCT/IB 00/00603

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
Y	<p>WO 97 37044 A (ASTRA AKTIEBOLAG) 9 October 1997 (1997-10-09)</p> <p>page 2, line 11 - line 25 page 3, line 12 -page 16, line 15 page 16, line 21 -page 18, line 10 page 33, line 33 -page 34, line 14 page 64, line 22 - line 30</p>	<p>1-3, 7-10, 14-20, 25,26, 30-38, 42,43</p>
Y	<p>WO 98 26072 A (ELI LILLY AND COMPANY) 18 June 1998 (1998-06-18)</p> <p>page 2, line 1 - line 25 page 8, line 10 -page 9, line 2</p>	<p>1,2,5, 7-9,12, 14-19, 22,25, 28, 30-37, 40,42,43</p>
Y	<p>EP 0 786 519 A (HUMAN GENOME SCIENCES, INC.) 30 July 1997 (1997-07-30)</p> <p>page 5, line 41 -page 7, line 7</p>	<p>1,2,4, 7-9,11, 14-19, 21,25, 27, 30-37, 39,42,43</p>
Y	<p>BARTEL ET AL: "A PROTEIN LINKAGE MAP OF ESCHERICHIA COLI BACTERIOPHAGE T7" NATURE GENETICS,US,NEW YORK, NY, vol. 12, no. 12, January 1996 (1996-01), pages 72-77, XP002119798 ISSN: 1061-4036 the whole document</p>	<p>1,2,6-9, 13-19, 23-25, 28-37, 41-43</p>
A	<p>MICHELINE FROMONT-RACINE ET AL.: "Toward a functional analysis of the yeast genome through exhaustive two-hybrid screens" NATURE GENETICS, vol. 16, July 1997 (1997-07), pages 277-282, XP002100296 the whole document</p>	<p>1-43</p>

-/-

INTERNATIONAL SEARCH REPORT

International Application No

PCT/IB 00/00603

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
A	ROBERT M FREDERCKSON: "Macromolecular matchmaking: advances in two-hybrid and related technologies" CURRENT OPINION IN BIOTECHNOLOGY, vol. 9, no. 1, February 1998 (1998-02), pages 90-96, XP002127445 abstract page 90, left-hand column, paragraph 2 -right-hand column, paragraph 1 page 93, right-hand column, paragraph 2 -page 94, right-hand column, paragraph 1 -----	1-43
A	WO 96 32503 A (THE GENERAL HOSPITAL CORPORATION) 17 October 1996 (1996-10-17) page 4, line 10 -page 7, line 23 page 18, line 28 -page 20, line 33 page 28, line 28 - line 34 page 29, line 14 -page 30, line 16 page 38, line 29 -page 39, line 25 page 43, line 34 -page 45, line 9 page 57, line 18 -page 62, line 4 page 78, line 19 -page 79, line 4 -----	1-43
A	JEAN-F. TOMB ET AL. : "The complete genome sequence of the gastric pathogen Helicobacter pylori" NATURE, vol. 388, 7 August 1997 (1997-08-07), pages 539-547, XP002062106 LONDON GB cited in the application table 2 -----	44-47, 55-58, 76,77, 79-87
X	-& DATABASE EMBL 'Online! Accession number 025047, 1 January 1998 (1998-01-01) XP002148640 the whole document -----	59-75, 83-87

INTERNATIONAL SEARCH REPORT

International application No.
PCT/IB 00/00603

Box I Observations where certain claims were found unsearchable (Continuation of item 1 of first sheet)

This International Search Report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☐ Claims Nos.:
because they relate to subject matter not required to be searched by this Authority, namely:

2. ☐ Claims Nos.:
because they relate to parts of the International Application that do not comply with the prescribed requirements to such an extent that no meaningful International Search can be carried out, specifically:

3. ☐ Claims Nos.:
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

Box II Observations where unity of invention is lacking (Continuation of item 2 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:

see additional sheet

1. ☐ As all required additional search fees were timely paid by the applicant, this International Search Report covers all searchable claims.

2. ☐ As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.

3. ☒ As only some of the required additional search fees were timely paid by the applicant, this International Search Report covers only those claims for which fees were paid, specifically claims Nos.:

1-43, 53, 54, 79, 80 and partially 44-47, 51, 55-57, 81-87 (inventions 1, 30, 32 and 33)

4. ☐ No required additional search fees were timely paid by the applicant. Consequently, this International Search Report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:

Remark on Protest

- ☐ The additional search fees were accompanied by the applicant's protest.
- ☒ No protest accompanied the payment of additional search fees.

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

This International Searching Authority found multiple (groups of) inventions in this international application, as follows:

1. Claims: 1-43

Method for producing a collection of recombinant cell clones usable for two-hybrid systems using genomic DNA from a prokaryotic micro-organism; collection of cell clones so produced; use thereof in yeast two-hybrid systems, kit therefore and recombinant diploid yeast cell so obtained.

2. Claims: Partially 44-47, 51, 55-77, 81-87

Set of two polynucleotide and fragments thereof encoding polypeptide HP0047 of the left column of table I and polynucleotides and fragments thereof encoding interacting ORFs HP0047, HP0048 and HP0695 of the right column of table I; set of two corresponding polypeptides; protein-protein interaction and corresponding complex; computable readable medium having stored such interaction; use of such interacting polypeptides for identifying "selecting interacting domains SID" and SID of SEQ ID NO:68, 70, 72 of Table II and encoding polynucleotides of SEQ ID NO:67, 69, 71 of Table III and homologs thereof; uses thereof as primer or probe; vectors and host cells comprising the same; uses thereof for producing the polypeptides and polypeptides so obtained; uses of the polypeptides in screening assays for for identifying agents capable of modulating such protein-protein interaction; kit therefore and modulator agent so obtained; use of the polypeptides for the modulation of *Helicobacter pylori*'s protein interaction; use for the production of antibodies and antibody so obtained; pharmaceutical compositions comprising any of the above mentioned polynucleotides, polypeptides, vectors, host cells, modulators and antibodies.

3. Claims: Partially 44-47, 51, 55-77, 81-87

Idem as subject 2 for polypeptide HP0061 of the left column of table I and polypeptides HP0066, HP0978, and HP1409 of the right column of Table I; SID of SEQ ID NO:82, 84 and 86 of Table II and encoding polynucleotides of SEQ ID NO:81, 83 and 85 of Table III

4. Claims: Partially 44-47, 51, 55-77, 81-87

Idem as subject 2 for polypeptide HP0064 of the left column of table I and polypeptide HP0063 of the right column of Table I; SID of SEQ ID NO:88 of Table II and encoding polynucleotide of SEQ ID NO:87 of Table III

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

5. Claims: Partially 44-47, 51, 55-77, 81-87

Idem as subject 2 for polypeptide HP0066 of the left column of table I and polypeptide HP0066 of the right column of Table I; SID of SEQ ID NO:76 of Table II and encoding polynucleotide of SEQ ID NO:75 of Table III

6. Claims: Partially 44-47, 51, 55-77, 81-87

Idem as subject 2 for polypeptide HP0067 of the left column of table I and polypeptides HP0069, HP0609, HP0768, HP0770 and HP0956 of the right column of Table I; SID of SEQ ID NO:196, 198, 200, 202 and 204 of Table II and encoding polynucleotides of SEQ ID NO:195, 197, 199, 201 and 203 of Table III

7. Claims: Partially 44-47, 51, 55-77, 81-87

Idem as subject 2 for polypeptide HP0068 of the left column of table I and polypeptides HP0070 and HP0118 of the right column of Table I; SID of SEQ ID NO:64 and 66 of Table II and encoding polynucleotides of SEQ ID NO:63 and 65 of Table III

8. Claims: Partially 44-47, 51, 55-77, 81-87

Idem as subject 2 for polypeptide HP0069 of the left column of table I and polypeptide HP0067 of the right column of Table I; SID of SEQ ID NO:74 of Table II and encoding polynucleotide of SEQ ID NO:73 of Table III

9. Claims: Partially 44-47, 51, 55-77, 81-87

Idem as subject 2 for polypeptide HP0070 of the left column of table I and polypeptides HP0068 and HP0070 of the right column of Table I; SID of SEQ ID NO:262 and 264 of Table II and encoding polynucleotides of SEQ ID NO:261 and 263 of Table III

10. Claims: Partially 44-47, 51, 55-77, 81-87

Idem as subject 2 for polypeptide HP0071 of the left column of table I and polypeptides HP0278, HP0417, HP0570, HP0775, HP1340 and HP1409 of the right column of Table I; SID of SEQ ID NO:142, 144, 146, 148, 150 and 152 of Table II and encoding polynucleotides of SEQ ID NO:141, 143, 145, 147, 149 and 151 of Table III

11. Claims: Partially 44-47, 51, 55-77, 81-87

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

Idem as subject 2 for polypeptide HP0072 of the left column of table I and polypeptide HP1489 of the right column of Table I; SID of SEQ ID NO:256 of Table II and encoding polynucleotide of SEQ ID NO:255 of Table III

12. Claims: Partially 44-47, 51, 55-77, 81-87

Idem as subject 2 for polypeptide HP0073 of the left column of table I and polypeptides HP0073, HP0232, HP0259, HP0067, HP0232 and HP0705 of the right column of Table I; SID of SEQ ID NO:154, 156, 158, 274, 276 and 278 of Table II and encoding polynucleotides of SEQ ID NO:153, 155, 157, 273, 275 and 277 of Table III

13. Claims: Partially 44-47, 51, 55-77, 81-87

Idem as subject 2 for polypeptide HP0268 of the left column of table I and polypeptide HP1198 of the right column of Table I; SID of SEQ ID NO:78 of Table II and encoding polynucleotide of SEQ ID NO:77 of Table III

14. Claims: Partially 44-47, 51, 55-77, 81-87

Idem as subject 2 for polypeptide HP0289 of the left column of table I and polypeptides HP0289, HP0887, HP0922, HP1038, HP1543, HP0610 and HP1355 of the right column of Table I; SID of SEQ ID NO:44, 46, 48, 50, 52, 54, 56, 58, 60 and 62 of Table II and encoding polynucleotides of SEQ ID NO:43, 45, 47, 49, 51, 53, 55, 57 and 61 of Table III

15. Claims: Partially 44-47, 51, 55-77, 81-87

Idem as subject 2 for polypeptide HP0311 of the left column of table I and polypeptide HP0312 of the right column of Table I; SID of SEQ ID NO:194 of Table II and encoding polynucleotide of SEQ ID NO:193 of Table III

16. Claims: Partially 44-47, 51, 55-77, 81-87

Idem as subject 2 for polypeptide HP0338 of the left column of table I and polypeptides HP0132 and HP0337 of the right column of Table I; SID of SEQ ID NO:166 and 168 of Table II and encoding polynucleotides of SEQ ID NO:165 and 167 of Table III

17. Claims: Partially 44-47, 51, 55-77, 81-87

Idem as subject 2 for polypeptide HP0391 of the left column

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of table I and polypeptides HP0392 and HP0392 of the right column of Table I; SID of SEQ ID NO:258 and 260 of Table II and encoding polynucleotides of SEQ ID NO:257 and 259 of Table III

18. Claims: Partially 44-47, 51, 55-77, 81-87

Idem as subject 2 for polypeptide HP0691 of the left column of table I and polypeptides HP0692 and HP1362 of the right column of Table I; SID of SEQ ID NO:266 and 268 of Table II and encoding polynucleotides of SEQ ID NO:265 and 267 of Table III

19. Claims: Partially 44-47, 51, 55-77, 81-87

Idem as subject 2 for polypeptide HP0697 of the left column of table I and polypeptides HP0012, HP0048, HP0558, HP0599, HP0696, HP0684, HP1037, HP1038, HP1299 and HP1576 of the right column of Table I; SID of SEQ ID NO:222, 224, 226, 228, 230, 232, 234, 236, 238 and 240 of Table II and encoding polynucleotides of SEQ ID NO:221, 223, 225, 227, 229, 231, 233, 235, 237 and 239 of Table III

20. Claims: Partially 44-47, 51, 55-77, 81-87

Idem as subject 2 for polypeptide HP0776 of the left column of table I and polypeptides HP0067, HP0278, HP1378, and HP1409 of the right column of Table I; SID of SEQ ID NO:214, 216, 218 and 220 of Table II and encoding polynucleotides of SEQ ID NO:213, 215, 217 and 219 of Table III

21. Claims: Partially 44-47, 51, 55-77, 81-87

Idem as subject 2 for polypeptide HP0797 of the left column of table I and polypeptides HP0289, HP0887, HP1349, HP1377 and HP1409 of the right column of Table I; SID of SEQ ID NO:184, 186, 188, 190 and 192 of Table II and encoding polynucleotides of SEQ ID NO:183, 185, 187, 189 and 191 of Table III

22. Claims: Partially 44-47, 51, 55-77, 81-87

Idem as subject 2 for polypeptide HP0800 of the left column of table I and polypeptides HP0433, HP0687, HP0800, HP0801, HP0924, HP1267 and HP1460 of the right column of Table I; SID of SEQ ID NO:10, 12, 14, 16, 18, 20 and 22 of Table II and encoding polynucleotides of SEQ ID NO:9, 11, 13, 15, 17, 19 and 21 of Table III

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23. Claims: Partially 44-47, 51, 55-77, 81-87

Idem as subject 2 for polypeptide HP0801 of the left column of table I and polypeptides HP0152, HP0800 and HP1513 of the right column of Table I; SID of SEQ ID NO:24, 26, and 28 of Table II and encoding polynucleotides of SEQ ID NO:23, 25 and 27 of Table III

24. Claims: Partially 44-47, 51, 55-77, 81-87

Idem as subject 2 for polypeptide HP0868 of the left column of table I and polypeptides HP0088, HP0327, HP0869, and HP1142 of the right column of Table I; SID of SEQ ID NO:2, 4, 6 and 8 of Table II and encoding polynucleotides of SEQ ID NO:1, 3, 5 and 7 of Table III

25. Claims: Partially 44-47, 51, 55-77, 81-87

Idem as subject 2 for polypeptide HP0874 of the left column of table I and polypeptide HP0875 of the right column of Table I; SID of SEQ ID NO:254 of Table II and encoding polynucleotide of SEQ ID NO:253 of Table III

26. Claims: Partially 44-47, 51, 55-77, 81-87

Idem as subject 2 for polypeptide HP0875 of the left column of table I and polypeptide HP0874 of the right column of Table I; SID of SEQ ID NO:212 of Table II and encoding polynucleotide of SEQ ID NO:211 of Table III

27. Claims: Partially 44-47, 51, 55-77, 81-87

Idem as subject 2 for polypeptide HP0887 of the left column of table I and polypeptides HP0459, HP0610, HP0699, HP0887, HP1157, HP1460, and HP1464 of the right column of Table I; SID of SEQ ID NO:30, 32, 34, 36, 38, 40, 42, 242, 244, 246 and 248 of Table II and encoding polynucleotides of SEQ ID NO:29, 31, 33, 35, 37, 39, 40, 41, 241, 243, 245 and 247 of Table III

28. Claims: Partially 44-47, 51, 55-77, 81-87

Idem as subject 2 for polypeptide HP0935 of the left column of table I and polypeptides HP0072, HP0528 and HP0657 of the right column of Table I; SID of SEQ ID NO:160, 162 and 164 of Table II and encoding polynucleotides of SEQ ID NO:159, 161 and 163 of Table III

29. Claims: Partially 44-47, 51, 55-77, 81-87

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Idem as subject 2 for polypeptide HP0978 of the left column of table I and polypeptides HP0979 and HP1583 of the right column of Table I; SID of SEQ ID NO:138 and 140 of Table II and encoding polynucleotides of SEQ ID NO:137 and 139 of Table III

30. Claims: Partially 44-47, 51, 55-77, 81-87

Idem as subject 2 for polypeptide HP1032 of the left column of table I and polypeptides HP0643, HP0818, HP1122, HP1198 and HP1316 of the right column of Table I; SID of SEQ ID NO:122, 124, 126, 128 and 130 of Table II and encoding polynucleotides of SEQ ID NO:121, 123, 125, 127 and 129 of Table III

31. Claims: Partially 44-47, 51, 55-77, 81-87

Idem as subject 2 for polypeptide HP1067 of the left column of table I and polypeptide HP0392 of the right column of Table I; SID of SEQ ID NO:210 of Table II and encoding polynucleotide of SEQ ID NO:209 of Table III

32. Claims: 53, 54, 79, 80 and partially 44-47, 51, 55-77, 81-87

Idem as subject 2 for polypeptide HP1198 of the left column of table I and polypeptides HP0088, HP0268, HP0293, HP0452, HP0705, HP0775, HP0965, HP1032, HP1114, HP1124, HP1198, HP1274, HP1378, HP1411, HP1541 and HP1218 of the right column of Table I; SID of SEQ ID NO:90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 270 and 272 of Table II and encoding polynucleotides of SEQ ID NO:89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, 269 and 271 of Table III

33. Claims: Partially 44-47, 51, 55-77, 81-87

Idem as subject 2 for polypeptide HP1230 of the left column of table I and polypeptides HP1230 and HP1529 of the right column of Table I; SID of SEQ ID NO:132, 134 and 136 of Table II and encoding polynucleotides of SEQ ID NO:131, 133 and 135 of Table III

34. Claims: Partially 44-47, 51, 55-77, 81-87

Idem as subject 2 for polypeptide HP1231 of the left column of table I and polypeptide HP1247 of the right column of Table I; SID of SEQ ID NO:120 of Table II and encoding

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polynucleotide of SEQ ID NO:119 of Table III

35. Claims: Partially 44-47, 51, 55-77, 81-87

Idem as subject 2 for polypeptide HP1244 of the left column of table I and polypeptides HP0857 and HP1246 of the right column of Table I; SID of SEQ ID NO:206 and 208 of Table II and encoding polynucleotides of SEQ ID NO:205 and 207 of Table III

36. Claims: Partially 44-47, 51, 55-77, 81-87

Idem as subject 2 for polypeptide HP1246 of the left column of table I and polypeptides HP0121, HP0326, HP0407, HP0886, HP1035, HP1244 and HP1460 of the right column of Table I; SID of SEQ ID NO:170, 172, 174, 176, 178, 180 and 182 of Table II and encoding polynucleotides of SEQ ID NO:169, 171, 173, 175, 177, 179 and 181 of Table III

37. Claims: Partially 44-47, 51, 55-77, 81-87

Idem as subject 2 for polypeptide HP1247 of the left column of table I and polypeptides HP1231 and HP1353 of the right column of Table I; SID of SEQ ID NO:250 and 252 of Table II and encoding polynucleotides of SEQ ID NO:249 and 251 of Table III

38. Claims: 52, 78 and partially 44-47, 51, 55-77, 81-87

Idem as subject 2 for polypeptide HP1293 of the left column of table I and polypeptide HP1198 of the right column of Table I; SID of SEQ ID NO:80 of Table II and encoding polynucleotide of SEQ ID NO:79 of Table III

39. Claims: 48 and partially 44-46, 51, 55-57-59, 76, 77, 81, 82, 84-87

Set of two polynucleotides and fragments thereof encoding two Staphylococcus polypeptides; set of two corresponding polypeptides, protein-protein interaction and corresponding complex; computable readable medium having stored such interaction; use of such interacting polypeptides for identifying "selecting interacting domains SID" and polynucleotide encoding SID; uses of the polypeptides in screening assays for identifying agents capable of modulating such protein-protein interaction; kit therefore and modulator agent so obtained; use of the polypeptides in the preparation of antibodies; antibodies so produced and pharmaceutical compositions comprising any of the above

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mentioned polypeptides, polynucleotides, modulators or antibodies.

40. Claims: 49 and partially 44-46, 51, 55-57-59, 76, 77, 81, 82, 84-87

Idem as subject 39 for Streptococcus pneumoniae polypeptides and polynucleotides.

41. Claims: 50 and partially 44-46, 51, 55-57-59, 76, 77, 81, 82, 84-87

Idem as subject 39 for Escherichia coli polypeptides and polynucleotides.

42. Claims: Partially 44-47, 51, 55-77, 81-87

Idem as subject 2 interacting polypeptides not covered by the above mentioned subjects

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